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(54) Title: MODULATING DEVELOPMENTAL PATHWAYS IN PLANTS

(57) Abstract: The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in Arabidopsis thaliana or other plants. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein.

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Title: Modulating developmental pathways in plants.

5

The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The different domains of RKS gene products essentially have the following functions: The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine / proline rich region. The next domain displays all the characteristics of a single transmembrane domain. At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062, WO 01/29240). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

35

Plant homologs of the Arabidopsis RKS genes can be found by comparison of various plant database (see also Table 2) and comprise amongst others:

- 5 Y14600|SBRLK1|*Sorghum bicolor*
BF004020|BF004020|EST432518 KV1 *Medicago truncatata*
AW934655|AW934655|EST353547 tomato
AW617954|AW617954|EST314028 *L. pennellii*
AA738544|AA738544|SbRLK2 *Sorghum bicolor*
- 10 AA738545|AA738545|SbRLK3 *Sorghum bicolor*
BG595415|BG595415|EST494093 cSTS *Solanum tuberosa*
AI896277|AI896277|EST265720 tomato
BF643238|BF643238|NF002H05EC1F1045
AA738546|AA738546|SbRLK4 *Sorghum bicolor*
- 15 BE658174|BE658174|GM700005A20D5 Gm-r1070 *Glycine max*
BF520845|BF520845|EST458318 DSIL *Medicago truncata*
AC069324|AC069324|*Oryza sativa*
AW761055|AW761055|s170d06.y1 Gm-cl027 *Glycine max*
BE352622|BE352622|WHE0425_G11_M21ZS Wheat
- 20 BG647340|BG647340|EST508959 HOGA *Medicago truncata*
AY028699|AY028699|*Brassica napus*
AW666082|AW666082|sk31h04.y1 Gm-cl028 *Glycine max*
AA738547|AA738547|SbRLK5 *Sorghum bicolor*
BG127658|BG127658|EST473220 tomato
- 25 L27821|RICPRKI|*Oryza sativa*
BG238468|BG238468|sab51a09.y1 Gm-cl043 *Glycine max*
BG441204|BG441204|GA_Ea0012C15f *Gossypium arbo.*
AW667985|AW667985|GA_Ea0012C15 *Gossypium arbore.*
AW233982|AW233982|sf32g05.y1 Gm-cl028 *Glycine max*
- 30 AP003235|AP003235|*Oryza sativa*
BF460294|BF460294|074A05 Mature tuber
AY007545|AY007545|*Brassica napus*
AC087544|AC087544|*Oryza sativa*
AB041503|AB041503|*Populus nigra*

35

The invention furthermore relates to modifying ELS genes or gene products or functional equivalents thereof which are for example derived from at least two different genes in the

40 Arabidopsis genome. They show high homology on protein level

with the corresponding transmembrane RKS gene products.
However, they lack a transmembrane domain while they do
contain a signaling sequence at the N-terminal end. Therefore
these proteins are thought to be positioned within vesicles
5 within the plant cell or at the outside of the plasma
membrane, within the cell wall of the plant cell. A number of
homologs have been detected in other plant species, such as:

- AF370543|AF370543|*Arabidopsis thaliana*
10 AF324989|AF324989|*Arabidopsis thaliana*
AV520367|AV520367|*Arabidopsis thaliana*
AV553051|AV553051|*Arabidopsis thaliana*
BF642233|BF642233|NF050C09IN1F1069
AW559436|AW559436|EST314484 *DSIR Medicago truncata*
15 BG456991|BG456991|NF099F02PL1F1025
AW622146|AW622146|EST312944 tomato
BF260895|BF260895|HVSMEf0023D15f *Hordeum vulgare*
BE322325|BE322325|NF022E12IN1F1088
BG414774|BG414774|HVSMEk0003K21f *Hordeum vulgare*
20 BE460627|BE460627|EST412046 tomato
BI204894|BI204894|EST522934 cTOS *Lycopersicon esculentum*
BI205306|BI205306|EST523346 cTOS *Lycopersicon esculentum*
BI204366|BI204366|EST522406 cTOS *Lycopersicon esculentum*
AW443205|AW443205|EST308135 tomato
25 AW031110|AW031110|EST274417 tomato
BI180080|BI180080|EST521025 cSTE *Solanum tuberosa*
BF644761|BF644761|NF015A11EC1F1084
AV526127|AV526127|*Arabidopsis thaliana*
AV556193|AV556193|*Arabidopsis thaliana*
30 BE203316|BE203316|EST403338 KV1 *Medicago truncatata*.
AW649615|AW649615|EST328069 tomato
BE512465|BE512465|946071E06
BI204917|BI204917|EST522957 cTOS *Lycopersicon esculentum*
BG590749|BG590749|EST498591
35 BG648725|BG648725|EST510344 HOGA *Medicago truncata*
BG648619|BG648619|EST510238 HOGA *Medicago truncata*
BG597757|BG597757|EST496435 cSTS *Solanum tuberosa*
AW221939|AW221939|EST298750 tomato
BE704836|BE704836|Sc01_
40 BG124409|BG124409|EST470055 tomato

- BF051954|BF051954|EST437120 tomato
BG320355|BG320355|Zm03_05h01_Zea mays
AV526624|AV526624|*Arabidopsis thaliana*
AW933960|AW933960|EST359803 tomato
- 5 AW221278|AW221278|EST297747 tomato
BE405514|BE405514|WHE1212_C01_F02ZS Wheat
BG314461|BG314461|WHE2495_A12_A23ZS *Triticum*
BF258673|BF258673|HVSMEf0016G01f *Hordeum vulgare*
BG262637|BG262637|WHE0938_E03_I06ZS Wheat
- 10 AW030188|AW030188|EST273443 tomato
BG653580|BG653580|sad76b11.y1 Gm-c1051 *Glycine max*
BG319729|BG319729|Zm03_05h01_A Zm03_Zea mays
BF053590|BF053590|EST438820 potato
BE454808|BE454808|HVSMEh0095C03f *Hordeum vulgare*
- 15 BI075801|BI075801|IP1_21_D05.b1_A002
BE367593|BE367593|PI1_9_F02.b1_A002 *Sorghum bicolor*
2e-074 BF260080|BF260080|HVSMEf0021A22f *Hordeum vulgare*
BF627921|BF627921|HVSMEb0006I23f *Hordeum vulgare*
BG598491|BG598491|EST503391 cSTS *Solanum tuberosa*
- 20 AW038168|AW038168|EST279825 tomato
BG343258|BG343258|HVSMEg0005D23f *Hordeum vulgare*
AW925684|AW925684|HVSMEg0005D23 *Hordeum vulgare*
BG416093|BG416093|HVSMEk0009L18f *Hordeum vulgare*
AW683370|AW683370|NF011C09LF1F1069
- 25 BE420108|BE420108|WWS020.C1R000101 ITEC WWS Wheat
AW350720|AW350720|GM210009A10F4 Gm-r1021 *Glycine max*
AW616564|AW616564|EST322975 *L. Hirsutum trichome*
AW011134|AW011134|ST17B03 Pine
BF630746|BF630746|HVSMEb0013N06f *Hordeum vulgare*
- 30 AW926045|AW926045|HVSMEg0006C10 *Hordeum vulgare*
BE519800|BE519800|HV_CEb0021E12f *Hordeum vulgare*
BG343657|BG343657|HVSMEg0006C10f *Hordeum vulgare*
BG933682|BG933682|OV1_16_C09.b1_A002
BE433368|BE433368|EST399897 tomato
- 35 AW219797|AW219797|EST302279 tomato
BF629324|BF629324|HVSMEb0010N06f *Hordeum vulgare*
BE597128|BE597128|PI1_71_A07.g1_A002
AW220075|AW220075|EST302558 tomato
AW616639|AW616639|EST323050 *L. Hirsutum trichome*
- 40 BF645214|BF645214|NF032F11EC1F1094
AW924540|AW924540|WS1_70_H12.b1_A002

AI775448|AI775448|EST256548 tomato

AW983360|AW983360|HVSMEg0010F15f *Hordeum vulgare*

BF270171|BF270171|GA_Eb0007B13f *Gossypium arbor.*

BE919631|BE919631|EST423400 potato

5 AW037836|AW037836|EST279465 tomato

BF008781|BF008781|ss79h09.y1 Gm-c1064 *Glycine max*

BF254651|BF254651|HVSMEf0004K05f *Hordeum vulgare*

BE599797|BE599797|PI1_79_H01.g1_A002

BE599026|BE599026|PI1_86_E03.g1_A002

10 R89998|R89998|16353 Lambda-PRL2 *Arabidopsis*

BG841108|BG841108|MEST15-G02.T3 ISUM4-TN *Zea mays*

AW307218|AW307218|sf54c07.y1 Gm-c1009 *Glycine max*

AI496325|AI496325|sb05c09.y1 Gm-c1004 *Glycine max*

AJ277703|ZMA277703|*Zea mays*

15 AL375586|CNS0616P|*Medicago truncatula* EST

AW350549|AW350549|GM210009A10A12 Gm-r1021 *Glycine max*

BE125918|BE125918|DG1_59_F02.b1_A002

BF053901|BF053901|EST439131 potato

BE921389|BE921389|EST425266 potato

20 BE597551|BE597551|PI1_71_A07.b1_

BE360092|BE360092|DG1_61_C09.b1_A002

BE660084|BE660084|491 GmaxSC *Glycine max*

AJ277702|ZMA277702|*Zea mays*

- 25 The invention also relates to modifying SBP/SPL gene or products which represent a family of transcription factors with a bipartite nuclear localization signal (The SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE (SBP/SPL) gene family of *Arabidopsis thaliana*, Columbia ecotype). Upon activation
- 30 (probably by RKS mediated phosphorylation, the bipartite nuclear localization signal becomes linear and available for the nuclear translocation of the protein. Within the plant nucleus, the transcription factor regulates transcription by interaction with specific promoter elements. .In *Arabidopsis*
- 35 *thaliana*, this family is represented by at least 16 different members (see following list). In many other plant species, we also identified members of this transcription factor family (See list on page 7).

Functional interaction between RKS and SBP proteins was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter (data not shown). At the tip of double overexpressing plants, embryo structures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signalling cascade, resulting in the reprogramming of developmental fate of a determined meristem. (ref. dissertation:

<http://www.ub.uni-koeln.de/ediss/archiv/2001/11w1204.pdf>;

Plant Journal 1997: 12, 2 367-377; Mol. Gen. Genet. 1996: 250, 7-16; Gene 1999, 237, 91-104, Genes and Development 1997: 11, 616-628), Proc. Natl. Acad. Sci. USA 1998: 95, 10306-10311; The Plant Journal 2000: 22, 523-529; Science 1997: 278, 1963-1965; Plant Physiol. Biochem. 2000: 38, 789-796; Cell 1996: 84, 61-71; Annu. Rev. Plant Physiol. Plant Mol. Biol. 1999: 50, 505-537

name	genetic code
ATSPL1	At2g47070*
ATSPL2	At5g43270
ATSPL3	At2g33810*
ATSPL4	At1g53160*
ATSPL5	At3g15270
ATSPL6	At1g69170
ATSPL7	At5g18830
ATSPL8	At1g02065
ATSPL9	At2g42200*
ATSPL10	At1g27370*
ATSPL11	At1g27360*
ATSPL12	At3g60030
ATSPL13	At5g50570
ATSPL14	At1g20980
ATSPL15	At3g57920
ATSPL16	At1g76580

* annotation in database not complete and/or correct

In many other plant species, we identified members of this transcription factor family, plant homologs of the Arabidopsis SBP/SPL proteins are for example:

- 5 AB023037|AB023037|*Arabidopsis thaliana*
BG789832|BG789832|sae56b07.y1 Gm-c1051 *Glycine max*
BG123992|BG123992|EST469638 tomato
BG595750|BG595750|EST494428 cSTS *Solanum tuberosum*
AF370612|AF370612|*Arabidopsis thaliana*
- 10 BF728335|BF728335|1000060H02.x1 1000 - *Zea mays*
X92079|AMSBP2|*A.majus*
AW331087|AW331087|707047A12.x1 707 - Mixed adult... 128 *zea mays*
AJ011643|ATH011643|*Arabidopsis thaliana*
L34039|RICRMSOA|*Oryza sativa*
- 15 AJ011638|ATH011638|*Arabidopsis thaliana*
AJ011639|ATH011639|*Arabidopsis thaliana*
AJ132096|ATH132096|*Arabidopsis thaliana*
BF482644|BF482644|WHE2301-2304_A21_A21ZS Wheat
BF202242|BF202242|WHE0984_D01_G02ZS Wheat
- 20 BE057470|BE057470|sm58e10.y1 Gm-c1028 *Glycine max*
AJ011628|ATH011628|*Arabidopsis thaliana*
AJ011629|ATH011629|*Arabidopsis thaliana*
AJ011617|ZMA011617|*Zea mays*
AJ011637|ATH011637|*Arabidopsis thaliana*
- 25 AJ011622|AMA011622|*Antirrhinum majus*
AJ011621|AMA011621|*Antirrhinum majus*
AJ011635|ATH011635|*Arabidopsis thaliana*
AJ011623|AMA011623|*Antirrhinum majus*
BF650908|BF650908|NF098D09EC1F1076
- 30 AJ242959|ATH242959|*Arabidopsis thaliana*
Y09427|ATSPL3|*A.thaliana* mRNA
AJ011633|ATH011633|*Arabidopsis thaliana*
AW691786|AW691786|NF044B06ST1F1000
BE058432|BE058432|sn16a06.y1 Gm-c1016 *Glycine max*
- 35 AW728623|AW728623|GA_Ea0017G06 *Gossypium arbore.*
BG442540|BG442540|GA_Ea0017G06f *Gossypium arbo.*
AJ011626|ATH011626|*Arabidopsis thaliana*
AJ011625|ATH011625|*Arabidopsis thaliana*
AI993858|AI993858|701515182 *A. thaliana*
- 40 BG593787|BG593787|EST492465 cSTS *Solanum tuberosum*
BF634536|BF634536|NF060C08DT1F1065 Drought *Medicago*

- BE806499|BE806499|ss59f10.y1 Gm-cl062 *Glycine max*
AW933950|AW933950|EST359793 tomato
AC008262|AC008262| *Arabidopsis*
B28493|B28493|T10A24TF TAMU *Arabidopsis thaliana*
- 5 AJ011644|ATH011644|*Arabidopsis thaliana*
AC018364|AC018364|*Arabidopsis thaliana*
AL092429|CNS00VLB|*Arabidopsis thaliana*
BE435668|BE435668|EST406746 tomato
BG097153|BG097153|EST461672 potato
- 10 BE440574|BE440574|sp47b09.y1 Gm-cl043 *Glycine max*
AI443033|AI443033|sa31a08.y1 Gm-cl004 *Glycine max*
U89496|ZMU89496|*Zea mays* liguleless1
AW433271|AW433271|sh54g07.y1 Gm-cl015 *Glycine max*
AW932595|AW932595|EST358438 tomato
- 15 AW096676|AW096676|EST289856 tomato
AJ011616|ZMA011616|*Zea mays*
AW036750|AW036750|EST252139 tomato
BF626329|BF626329|HVSMEa0018F24f *Hordeum vulgare*
AJ011614|ZMA011614|*Zea mays*
- 20 AJ011642|ATH011642|*Arabidopsis thaliana*
BE022435|BE022435|sm85h04.y1 Gm-cl015 *Glycine max*
X92369|AMSPB1|*A.majus*
AC015450|AC015450|*Arabidopsis thaliana*
AC079692|AC079692|*Arabidopsis thaliana*
- 25 AJ011632|ATH011632|*Arabidopsis thaliana*
AJ011631|ATH011631|*Arabidopsis thaliana*
BE455349|BE455349|HVSMEh0097E20f *Hordeum vulgare*
AJ242960|ATH242960|*Arabidopsis thaliana*
AJ011610|ATH011610|*Arabidopsis thaliana*
- 30 AJ132097|ATH132097|*Arabidopsis thaliana*
AL138658|ATT209|*Arabidopsis thaliana*
AJ011615|ZMA011615|*Zea mays*
BE499739|BE499739|WHE0975_ Wheat
AW398794|AW398794|EST309294 *L. pennellii*
- 35 AJ011618|ZMA011618|*Zea mays*
AW747167|AW747167|WS1_66_F11.b1_
AJ011577|ATH011577|*Arabidopsis thaliana*
AI992727|AI992727|701493410 *A. thaliana*
BE060783|BE060783|HVSMEg0013F15f *Hordeum vulgare*
- 40 BE804992|BE804992|ss34h10.y1 Gm-cl061 *Glycine max*
BE325341|BE325341|NF120H09ST1F1009

AC007369|AC007369|*Arabidopsis thaliana*

AJ011619|ZMA011619|*Zea mays*

BI099345|BI099345|IP1_37_H10.b1_A002

BI071295|BI071295|C054P79U *Populus*

5 AZ920400|AZ920400|1006019G01.y2 1006 -

AZ919034|AZ919034|1006013G02.x3 1006 -

BE805023|BE805023|ss35d09.y1 Gm-cl061 *Glycine max*

BG582086|BG582086|EST483824 GVN *Medicago truncata*

AJ011609|ATH011609|*Arabidopsis thaliana*

10 BE023083|BE023083|sm90e08.y1 Gm-cl015 *Glycine max*

Furthermore, the invention relates to modifying NDR-NHL-genes or gene products. All proteins belonging to this family contain one (and sometimes even more than one) transmembrane domain. *Arabidopsis* contains a large number of NDR-NHL genes, such as:

20 aad21459, aaf18257, aac36175, k10d20 (position 40852-41619),
aad21460, cab78082, aad21461, aad42003, aaf02134, aaf187656,
aaf02133, cab43430, cab88990, cab80950, aad25632, aaf23842, all163812,
f20d21-35, t13m11-12, fle22-7, t23g18, f5d14-4266, t32f12-16, f11f19-
11, f11f19-12, f11f19-13, t20p8-13, f12k2, f23h14, k10d20-44043,
k10d20-12, t19f11-6, t19f11-5, t10d17-10, f22o6-150, f3d13-5, m3e9-
80, t25p22-30, mhf15-4, mhf15-5, mrn17-4, mlf18-9, mgn6-11994, mjj3-
9667, f14f18-60, At1g17620 F11A6, At5g11890 , At2g27080 , At5g36970 ,
25 mlf18 , At1g65690 F1E22 , At4g01110 F2N1 , At2g35980 f11f19 ,
At4g01410 F3D13 , At1g54540 F20D21 , At2g46300 t3f17 , At5g21130 ,
At3g11650 T19F11 , At5g06320 MHF15 , At5g06330 MHF15 , At2g01080
f15b18 , At2g35460 t32f12 , At2g27260 f12k2 , At2g35970 f11f19 ,
At5g53730 MGN6 , At5g22870 MRN17 , At4g09590 , At3g54200 , At1g08160
30 T6D22 , At5g22200 , At3g52470 , At2g35960 f11f19 , At3g52460 ,
At5g56050 MDA7, At3g20590 K10D20 , At1g61760 T13M11 , At3g20600
K10D20 , At1g13050 F3F19 , At3g11660 T19F11 , At3g44220 , At1g64450
F1N19 , At3g26350 F20C19 C , At4g05220 , At5g45320 K9E15 ,
At4g23930 , At4g13270 , At4g39740 , At1g45688 F2G19 W , At5g42860
35 MBD2 , At1g32270 F27G20 , At4g30660 , At2g45430 f4123 , At4g30650 ,
At1g69500 F10D13

and

40 ndr1, At2g27080; T20P8.13, At5g21130, At1g65690, At5g36970,

At1g54540, At5g06320, At5g11890, At1g17620, At3g11650, At2g22180,
At5g22870, At2g35980, At2g46300, At4g05220, At2g35460, At2g27260,
At4g01410, At5g22200, At1g61760, At3g52470, At5g53730, At4g01110,
At2g35960, At3g52460, At4g09590, At2g35970, At3g26350, At3g11660,
5 At3g44220, At1g08160, At2g01080, At5g06330, At5g56050, At3g20600,
NDR1, At3g54200, At3g20590, At4g39740, At1g32270 syntaxin, putative,
At1g13050, At5g45320, At3g20610, At4g26490, At5g42860, At1g45688,
At4g26820

10 NDR-NHL genes belong to a large family of which one of the
first identified is the defence-associated gene HIN1 (Harpin-
induced gene). HIN1 is transcriptionally induced by harpins
and bacteria, that elicit hypersensitive responses in tobacco.
It is thus believed that the genes of the invention also play
15 arole in the hypersensitive reaction. Especially (see also
chapter 8) since the genes of the invention bear relation to
brassinoid-like responses and since brassinoid pathway
compounds have been found to interact in this same defence
system in plants. Other plant species also contain members of
20 this large gene family, such as:

Plant homologs of the *Arabidopsis* NDR/NHL genes:

25 BG582276|BG582276|EST484016 GVN *Medicago truncata*
AV553539|AV553539|*Arabidopsis thaliana*
AC069325|AC069325|*Arabidopsis thaliana*
AV526693|AV526693|*Arabidopsis thaliana*
BG583456|BG583456|EST485208 GVN *Medicago truncata*
30 AW267833|AW267833|EST305961 DSIR *Medicago truncata*
BE997791|BE997791|EST429514 GVSN *Medicago truncata*
BG580928|BG580928|EST482657 GVN *Medicago truncata*
BF520916|BF520916|EST458389 DSIL *Medicago truncata*
AV544651|AV544651|*Arabidopsis thaliana*
35 AV543762|AV543762|*Arabidopsis thaliana*
AW559665|AW559665|EST314777 DSIR *Medicago truncata*
BG581012|BG581012|EST482741 GVN *Medicago truncata*
AV552164|AV552164|*Arabidopsis thaliana*
BE999881|BE999881|EST431604 GVSN *Medicago truncata*
40 AW031098|AW031098|EST274405 tomato

- AI998763|AI998763|701546833 *A. thaliana*
AW219286|AW219286|EST301768 tomato
BE124562|BE124562|EST393597 *GVN Medicago truncata*
AV540371|AV540371|*Arabidopsis thaliana*
- 5 AV539549|AV539549|*Arabidopsis thaliana*
BG647432|BG647432|EST509051 *HOGA Medicago truncata*
BE434210|BE434210|EST405288 tomato
BG725849|BG725849|sae42g02.y1 *Gm-cl051 Glycine max*
AP003247|AP003247|*Oryza sativa*
- 10 BE348073|BE348073|sp11a11.y1 *Gm-cl042 Glycine max*
AW508383|AW508383|si40c06.y1 *Gm-r1030 Glycine max*
AI856504|AI856504|sb40b07.y1 *Gm-cl014 Glycine max*
BE556317|BE556317|sq01b07.y1 *Gm-cl045 Glycine max*
AA713120|AA713120|32681 *Arabidopsis*
- 15 AV541531|AV541531|*Arabidopsis thaliana*
AI894456|AI894456|EST263911 tomato
AW704493|AW704493|sk53g11.y1 *Gm-cl019 Glycine max*
AW219298|AW219298|EST301780 tomato
BF425685|BF425685|ss03c11.y1 *Gm-cl047 Glycine max*
- 20 AV422557|AV422557|*Lotus japonicus*
BE190816|BE190816|sn79a08.y1 *Gm-cl038 Glycine max*
BG580331|BG580331|EST482056 *GVN Medicago truncata*
AV423251|AV423251|*Lotus japonicus*
AI896088|AI896088|EST265531 tomato
- 25 AV413427|AV413427|*Lotus japonicus*
AV426656|AV426656|*Lotus japonicus*
AV416256|AV416256|*Lotus japonicus*
AL385732|CNS0690I|*Medicago truncatula*
AB016877|AB016877|*Arabidopsis thaliana*
- 30 AV419449|AV419449|*Lotus japonicus*
AI486269|AI486269|EST244590 tomato
AV411690|AV411690|*Lotus japonicus*
AV419925|AV419925|*Lotus japonicus*
AV418222|AV418222|*Lotus japonicus*
- 35 AV409427|AV409427|*Lotus japonicus*
AC005287|AC005287|*Arabidopsis thaliana*
AV426716|AV426716|*Lotus japonicus*
AV411791|AV411791|*Lotus japonicus*
BG351730|BG351730|131E12 Mature tuber
- 40 BG046452|BG046452|saa54b12.y1 *Gm-cl060 Glycine max*
AI781777|AI781777|EST262656 tomato

- BE451428|BE451428|EST402316 tomato
AI772944|AI772944|EST254044 tomato
AI895510|AI895510|EST264953 tomato
AW030762|AW030762|EST274017 tomato
5 AW218859|AW218859|EST301341 tomato
BE203936|BE203936|EST396612 *KVO Medicago truncata*
AV410289|AV410289|*Lotus japonicus*
AW032019|AW032019|EST275473 tomato
AW030868|AW030868|EST274158 tomato
10 AV421824|AV421824|*Lotus japonicus*
BG646408|BG646408|EST508027 *HOGA Medicago truncata*
AF325013|AF325013|*Arabidopsis thaliana*
AC007234|AC007234|*Arabidopsis thaliana*
AW217237|AW217237|EST295951 tomato
15 AC034257|AC034257|*Arabidopsis thaliana*
AW625608|AW625608|EST319515 tomato
AW031064|AW031064|EST274371 tomato
AF370332|AF370332|*Arabidopsis thaliana*
AB006700|AB006700|*Arabidopsis thaliana*
20 AW035467|AW035467|EST281205 tomato
AL163812|ATF14F18|*Arabidopsis thaliana*
AI896652|AI896652|EST266095 tomato
AI730803|AI730803|BNLGH17970 Cotton
AW034775|AW034775|EST278811 tomato

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The invention provides the insight that RKS proteins or functional equivalents thereof play part in a signaling complex (herein also called the RKS signaling complex) comprising molecules of RKS proteins, ELS (Extracellular Like SERK) proteins, NDR/NHL proteins and SBP/SPL (Squamosa Binding Protein) proteins, and the corresponding protein ligands (see for example table 3) whereby each of these proteins interplay or act in such a way that modifying genes, or modifying expression of genes, encoding ELS, RKS, NDR/NHL or SBP/SPL, proteins or said ligands may lead to functionally equivalent results (Figure 5. Two-hybrid interaction experiments have for example shown in vitro interaction between RKS 0 and NDR0/NHL28 and members of the SBP/SPL family. Here we show that in vivo the individual components of this signaling

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complex are regulating identical processes, as based on functional genomics on transgenic plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex. ELS gene products
5 are derived from at least two different genes in the Arabidopsis genome. They show high homology on protein level with the corresponding transmembrane RKS gene products.

However, they lack a transmembrane domain while they do contain a signalling sequence at the N-terminal end. Therefore
10 these proteins are thought to be positioned within vesicles within the plant cell or at the outside of the plasma membrane, within the cell wall of the plant cell. A number of homologues have been detected in other plant species (see list on page 3). ELS proteins are involved in the heterodimerizing
15 complex with the RKS transmembrane receptor at the outer membrane site. ELS molecules are either in competition or collaboration with RKS molecules involved in the high affinity binding of the ligand. The signal transmitted from the ligand onto the RKS proteins is then transporter over the membrane
20 towards the N-terminal site of RKS protein, located on the other site of the membrane. The activation stage of the RKS molecule is changed, as a result of transphosphorylation by dimerizing receptor kinase dimerizing partners. Subsequently the signal is transmitted to other proteins, one family of
25 such proteins is defined as the SBP/SPL family of transcription factors, the other family of proteins is represented by the NDR/NHL members.

The different obvious phenotypes created by modifying the
30 RKS gene products could be effected by one process regulating all different effects in transgenic plants.

All the phenotypes observed can be effected by the process of brassinosteroid perception. In chapter 1, RKS genes
35 are clearly involved in plant size and organ size. Loss of RKS expression results in a dwarf phenotype, similar as observed with brassinosteroid synthesis mutants. It was already known in literature that the phenotypes observed from modifying the

RKS genes are also observed when modifying the brassinosteroid pathway genes and/or their regulation, thereby altering the amount and nature of the brassinosteroids in plants.

Literature which describes the phenotypic effects of modifying

- 5 teh brassinosteroid pathway can, amongst others, be found in:
Plant Journal 26: 573-582 2001; Plant Journal 1996 9(5) 701-713, genetic evidence for an essential role of
brassinosteroids in plant development; J. Cell Biochem Suppl. 21a 479 (1995) ; Mandava 1988 Plant growth-promoting
10 brassinosteroids, Ann. Rev. Plant. Physiol. Plant Mol. Biol. 39 23-52; Plant Physiol 1994 104: 505-513; Cell 85 (1996) 171-182; Clouse et al. 1993 J. Plant Growth Regul. 12 61-66;
Clouse and Sasse (1998) Annu. Rev. Plant Physiol. Plant Mol. Biol 49 427-451; Sasse, Steroidal Plant Hormones. Springer-
15 Verlag Tokyo pp 137-161 (1999).

It is thus believed, without being bound to any theory, that modification of the RKS genes will result in a modification of the brassinosteroid pathway, thereby giving the various phenotypes that are shown below.

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- "Functionally equivalent" as used herein is not only used to identify the functional equivalence of otherwise not so homologous genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins, but also means an equivalent gene or gene product of
25 genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins in *Arabidopsis Thaliana*, e.g. identifying a homologue found in nature in other plants or a homologue comprising a deliberate nucleic acid modification, such as a deletion, truncation, insertion, or deliberate codon substitution which may be made on
30 the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. Homology is generally over at least 50% of the full-length of the relevant sequence shown herein. As is well-understood,
35 homology at the amino acid level is generally in terms of amino acid similarity or identity. Similarity allows for "conservative variation", i. e. substitution of one

hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine. Deliberate amino acid substitution may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. In a preferred embodiment, all percentage homologies referred to herein refer to percentage sequence identity, e.g. percent (%) amino acid sequence identity with respect to a particular reference sequence can be the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, without considering any conservative substitutions as part of the sequence identity. Amino acid similarity or identity can be determined by genetic programs known in the art.

'Plant cell', as used herein, amongst others comprises seeds, suspension cultures, embryos, meristematic regions, callous tissues, protoplasts, leaves, roots, shoots, bulbs, gametophytes, sporophytes, pollen and microspores. A target plant to be modified according to the invention may be selected from any monocotyledonous or dicotyledonous plant species, such as for example ornamental plants, vegetables, arable crops etc. 'Dicotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has two or more free or fused cotyledons. 'Monocotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has one cotyledon. 'Angiospermae' or flowering plants are seed plants characterized by flowers as specialized organs of plant reproduction and by carpels covering the ovaries. Also included are gymnospermae. Gymnospermae are seed plants characterized by strobili as specialized organs for plant reproduction and by naked sporophylls bearing the male or female reproductive organs, for example woody plants. 'Ornamental'

plants are plants that are primarily in cultivation for their habitus, special shape, (flower, foliage or otherwise) colour or other characteristics which contribute to human well being indoor as cut flowers or pot plants or outdoors in the man made landscape, for example bulbous plant species like *Tulipa*, *Freesia*, *Narcissus*, *Hyacinthus* etc. 'Vegetables' are plants that are purposely selected or bred for human consumption of foliage, tubers, stems, fruits, flowers or parts of them and that may need an intensive cultivation regime. 'Arable crops' are generally purposely bred or selected for human objectivity's (ranging from direct or indirect consumption, feed or industrial applications such as fibers) for example soybean, sunflower, corn, peanut, maize, wheat, cotton, safflower and rapeseed.

The invention provides a method for modulating a developmental pathway of a plant comprising modifying a gene encoding for a gene product or protein belonging to a developmental cascade or signaling complex comprising modifying at least one gene encoding a gene product belonging to the complex of RKS proteins, ELS proteins, NDR/NHL proteins, SBP/SPL proteins and ligand proteins. In one embodiment, the invention provides a method for modulating or modifying organ size. Plant or plant organ size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex with a method according to the invention is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating

cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth,

5 proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Use of a method according to invention for elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase for example the size of plant
10 organs, the growth rate, the yield of harvested crop, the yield of total plant material or the total plant size. Decreasing the levels of endogenous RKS gene product is provided in order to decrease the size of plant organs, the growth rate, or the total plant size.

15 In another embodiment, the invention relates to cell division. The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery
20 are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides
25 herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and
30 RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an
35 eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes,

especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

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In a further embodiment, the invention relates to the regeneration of apical meristem. Modification the levels of different RKS and ELS genes within plants allows the initiation and / or outgrowth of apical meristems, resulting in the formation of large numbers of plantlets from a single source. A number of gene products that is able to increase the regeneration potential of plants is known already. Examples of these are KNAT1, cycD3, CUC2 and IPT. Here we show that modulation of the endogenous levels of RKS genes results in the formation of new shoots and plantlets in different plant species like *Nicotiana tabacum* and *Arabidopsis thaliana*. Herewith the invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating apical meristem formation, in particular wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof. A direct application of such a method according to the invention is the stable or transient expression of RKS and ELS genes or gene products in order to initiate vegetative reproduction. Regeneration can be induced after overexpression of for example RKS0 and ELS1; or by co-suppression of for example the endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or co-suppression of these RKS and ELS gene products can be either transient, or stable by integration of the corresponding expression cassettes in the plant genome. A further example of essentially identical functions for for example ELS1 and RKS0 overexpressing plants is for example shown in the detailed description, example 3, where both transgenic constructs are able to induce the

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regeneration capacity of in vitro cultured *Arabidopsis* callus.

Another example comprises functional interaction between RKS and SBP proteins which was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter. At the tip of double overexpressing plants, embryostructures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signaling cascade, resulting in the reprogramming of developmental fate of a determined meristem.

Furthermore, it is herein also shown that several RKS genes are able to regulate proper identity and development of meristems and primordia. The invention for example also relates to fasciation, Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific

promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type.

Identical phenotypes can be observed when transgenic plants are produced that contain the NHL10 cDNA under control of an enhanced 35S promoter. The resulting phenotype of the resulting flowers show that flower organ primordia are switched in identity, similar as observed for RKS10 and RKS13. These meristematic identity switches are normally never observed in *Arabidopsis* and the fact that two different classes of genes are able to display the same phenotypes in transgenic plants is a clear indication for a process in which both members of the RKS and the NDR/NHL families are involved. The invention also relates to root development. Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular

wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof.

Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

In a further embodiment, the invention relates to apical meristem identity. All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue

and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering. Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows the formation of completely new types of flowers and fused fruitstructures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

In another embodiment, the invention relates to male sterility. Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more

introduced gene products interfere with normal pollen initiation and development is therefore highly desired.

Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses

with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

Furthermore, surprisingly we observe that NDR NHL gene products share homology with the family of syntaxins, involved in vesicle transport, positioning of cell wall formation and cytokinesis.

Table 1

Homology between members of the syntaxin family and the NDR
NHL family

5 NHL10= At2g35980

maaeqplnga fygpsvpppa pkgyyrrghg rgcgccllsl fvkviisliv ilgvaalifw
livrpraikf hvtdasltrf dhtspdnir ynaltvpvr npnkriglyy drieahayye
gkrfstittlt pfyqghkntt vltptfqqn lvifnagqsr tlnerisgv ynieikfrlr
vrfklgdlkf rrikpkvdcddlrplstsn gttttstvf ikcdfdf

10

Atlg32270 syntaxin,

MVRSNDVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR FEATVYYMNO
RLGAVPMPLF YLGSKNTMLL RALFEGQTLV LLKGNERKKF EDDQKTGVYR IDVKLSINFR
VMVLHLVTWP MKPVVRCHLK IPLALGSSNS TGGHKKMLLI GQLVKDTSAN LREASETDHR
15 RDVAQSKKIA DAKLAKDFEA ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS
QEQRVLMESR QEIVLLDNE ISLNEARIEA REQIQEVKH QISEVMEMFK DLAVMVDHQG
TIDDIDEKID NLRSAQAQ GK SHLVKASNTQ GSNSLLFSC SLLFFFLSG DLCRCVCVGS
ENPRLNPTRR KAWCEEEDEE QKKKQKKKT MSEKRRREEK KVNKPNGFVF CVLGHK*

20

Below the homology is shown between NHL10 (Upper line) and a
syntaxin protein. (bottom line). The identical amino acids are
shown in the middle line.

25

IVRPAIKFHVTDASLTRFDHTSPDNILRYNLALTVPVRNPNKRIGLYYDRIEAAHAYYEG
VR KF V DA LT FD S N L Y L L RN IG YDR EA YY
MVRSNDVKFQVYDAELTHFDLESNNN-LQYSLNLSIRNSKSSIGIHYDRFEATVYYMN

30

KRFSTITLTPFYQGHKNTTVLTPTFQQNLVIFNAGQSRTLNAERISGVYNIEIKFRLRV
R FY G KNT L F GQ LV G VY I K
QRLGAVPMPLFYLGSKNTMLLRALFEGQTLVLLKGNERKKFEDDQKTGVYRIDVKLSINF

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RFKLGDLKFRRIPKPVDCDDLRLPLSTSNNGTTT
R L KP V C L PL T
RVMVLHLVTWPMKPVVRCH-LKIPALGSSNST

That syntaxins and NDR/NHL genes share large homology becomes even more clear when performing a database search using the following site:

http://mips.gsf.de/proj/thal/db/search/search_frame.html

5 searching for homologous sequences with the sequence At1g32270

gene code:

predicted function:

	At1g32270 syntaxin, putative	Syntaxin
10	At5g46860 syntaxin related protein	Syntaxin
	AtVam3p (gb AAC49823.1)	
	At4g17730 syntaxin	Syntaxin
	At5g16830 syntaxin homologue	Syntaxin
	At3g11650 unknown protein	Putative syntaxin
15	At2g35460 similar to harpin-induced protein	Putative syntaxin
	At5g06320 harpin-induced protein-like	Putative syntaxin
	At2g35980 similar to harpin-induced protein	Putative syntaxin
	At1g65690 hypothetical protein	NDR HNL
	At4g05220 putative protein	Putative syntaxin
20	At3g05710 putative syntaxin protein	Syntaxin
	AtSNAP33	
	At2g27080 unknown protein	NDR HNL
	At3g52470 putative protein	Putative syntaxin
	At1g61760 hypothetical protein	Putative syntaxin
25	At5g21130 putative protein	NDR HNL
	At3g52400 syntaxin-like protein synt4	Syntaxin
	At2g35960 putative harpin-induced protein	Putative syntaxin
	At5g06330 harpin-induced protein-like	Putative syntaxin
	At5g26980 tSNARE	Syntaxin
30	At5g36970 putative protein	Putative syntaxin
	At3g44220 putative protein	Putative syntaxin
	At3g03800 s-syntaxin-like protein	Syntaxin
	At2g35970 putative harpin-induced protein	Putative syntaxin
	At4g09590 putative protein	Putative syntaxin
35	At4g23930 putative protein	
	At1g61290 similar to syntaxin-related protein	Syntaxin
	At3g11660 unknown protein	Putative syntaxin
	At1g54540 hypothetical protein	Putative syntaxin
	At3g24350 syntaxin-like protein	Syntaxin
40	At5g22200 NDR1/HIN1-like	NDR HNL

	At1g11250 syntaxin-related protein At-SYR1	Syntaxin
	At5g53880	
	At3g11820 putative syntaxin	Syntaxin
	At3g54200	Putative syntaxin
5	At5g05760 t-SNARE SED5	Syntaxin
	At5g53730	Putative syntaxin
	At4g03330 SYR1-like syntaxin 1	Syntaxin
	At3g47910	
	At5g08080 syntaxin-like protein	Syntaxin
10	At5g11890	Putative syntaxin
	At1g17620	Putative syntaxin
	At2g22180	Putative syntaxin
	At5g22870	Putative syntaxin
	At2g46300	Putative syntaxin
15	At2g27260	Putative syntaxin
	At4g01410	Putative syntaxin
	At5g22200	Putative syntaxin
	At4g01110	Putative syntaxin
	At3g52460	Putative syntaxin
20	At3g26350	Putative syntaxin
	At1g08160	Putative syntaxin
	At2g01080	Putative syntaxin
	At5g56050	Putative syntaxin
	At3g20600	Putative syntaxin
25	At3g20590	Putative syntaxin
	At4g39740	Putative syntaxin
	At1g32270	Putative syntaxin
	At1g13050	Putative syntaxin
	At5g45320	Putative syntaxin
30	At3g20610	Putative syntaxin
	At4g26490	Putative syntaxin
	At5g42860	Putative syntaxin
	At1g45688	Putative syntaxin
	At4g26820	Putative syntaxin
35		

40 This observation provides the explanation for understanding
the mechanism by which the RKS / NDR-NHL complex functions.
Cell wall immobilized RKS gene products (containing the

extensin-like extracellular domain) respond to a local ligand signal, in combination with the heterodimerizing ELS protein (s) either as homodimers, as RKS heterodimers or in combination with the heterodimerizing ELS protein(s).

5 Predicted ligands for the RKS / ELS receptor binding consist of peptide ligands (based on the LRR ligand binding domain of this class of receptors). These ligands are normally produced as a pre pro protein. The N-terminal signal sequence is removed by the transport through the Golgi system and
10 allows modification of the ligand at this stage (e.g. glycosylation). The ligands can then be secreted after which further processing is possible (e.c. proteolytic cleavage, removal of sugar groups etc.) The resulting peptide, possible
15 transmembrane receptor complex with high affinity, resulting in transmission of the signal from the ligand through the transmembrane receptor component towards the other site of the membrane.

One class of ligands interacting with the RKS and / or ELS
20 receptors consists of the family of pre(pro)proteins shown hereunder in table 3.

Table 3 Ligands within the RKS signaling complex (herein also called RKS/ELS ligand proteins)

For each ligand (A to N) the genomic structure before splicing and processing 5'- towards 3' is given. Exons are indicated in large letters; introns and surrounding sequences (including leader 5'-and trailer sequences 3'-) are indicated in small letters.

Beneath each DNA sequence the amino acid sequence of the pre-pro-peptide is given. The first line represents the signal sequence

The second (set of) lines represents the pro-peptide.

The last line represents the conserved Cysteine motif.

A. At1g22690

```
1 attaaacgcc aaacactaca tctgtgtttt cgaacaatat tgcgtctgcg tttccttcat
61 ctatctctct cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac
121 ataaactacc aaagtatcaa gctaattgtaa aaattactct catttccacg taacaaattg
181 agttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcac
241 ctccgaaaaa aggyaaccac tcaaaactgt ttgcatatca aactccaaca ctttacagca
301 aatgcaatct ataactctgtg atttatccaa taaaaacctg tgatttatgt ttggctccag
361 cgatgaaagt ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa
421 gtagctgaaa tgtatctata taaagaatca tccacaagta ctattttcac acactacttc
481 aaaactacta ctcaagaaat ATGAAGAAGA TGAATGTGGT GGCTTTTGT ACCTGTATCA
541 TCTCTTTTCT TCTGCTTTCT CAGgtaaact gttaaaacca ttttcaagac taccttttct
601 ctatttcaga caaaccaaag taaaacaatg aaaaatctct ctggtctttc atagTACTT
661 GCAGAGTTGT CATCATCCAG CAACAATGAA ACTTCCTCTG TTTCTCAGgt aagagtgata
721 caaaaacata ctaaacaaac tttcaagaga gtaatatata aggaaatgtt ggcttctttt
781 ttttggttgc aatcagACGA ATGACGAGAA CCAACTGCG GCGTTAAGA GAACATACCA
841 CCATCGTCCA AGAATCAgtt agtctactct ttcaacactc taattccttt gttctaagta
901 ttttttttgc cccccacaac ctttttttta ttaaatgagc caatttttat agATTGTGGG
961 CATGCATGCG CAAGGAGATG CAGTAAGACA TCGAGGAAGA AAGTTGTGCA CAGAGCCTGT
1021 GGAAGTTGTT GTGCCAAGTG TCAGTGTGTG CCGCCGGGAA CCTCCGGCAA CACAGCATCA
1081 TGTCTTTGCT ACGCCAGTAT CCGTACACAT GGCAATAAAC TCAAATGTCC TTAAaagact
1141 tctcatttct caactatagt ctcatcttct gattatgttt cttcttttgt tatgttgcac
1201 gtgtgatgtg tgagcttatt attatgttga ttgttgacat aattcaacta tataatttgt
1261 atcgattccg aataataaga tgagtgtatt tattggctat taagtttttt tttttttttt
1321 ttgggcacaa tggctattaa gttttaaaca tctgatttta ttggttacia aaaacaacaa
1381 agtttcattt tcoatattaac acaaaatctc catatatatt accaaaccaa aaaaatacac
1441 aagggggaga gagaccaacg gttcttgggt cagagtgttc atcttgtttg agccgtcacc
1501 gtttcttaga cttaacagcc acaacacctt tataaagctt cagcgcgac ttcaacgcac
1561 ctgcgcgagg ccgagccacc ttattgtttg gatcaaacaa caaaacttct tcaaacgcac
1621 tcaatgccaa aggc
```

MKKMNVVAFVTLIISFLLSQVLA

ELSSSSNNETSSVSQTNDENQTAAFKRTYHHRPRIN

CGHACARRCSKTSRKVKCHRACGCCAKCQCVPPTSGNTASCPYASIRTHGNKLKCP*

B. At1g74670

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61 ttagtttgta tataatacag tagactaggg atccagttga gtttctttct ttattttgag
121 tttgtgttta tgtttgattt tacgttttta tatgtaaata agataattta cgaattatgg
181 ttttatttgg gtagaagttg tagaatgact taaacaatca agtggcagaa tgagatatat
241 aaagtaatat aatataatgta ccgttattaa cttattgtac atgtgaatga ggaagcttac
301 acacacacac cttctataaa tagctgacaa aactggttgt tacacacaac acattcataa
10 361 atctctcaaa gtaagaacta agagctttac tacagtccta ctctctacac atcttctctc
421 tctctcaaga gctagtcATG GCCAAACTCA TAACTTCTTT TCTCTTACTC ACAATTTTAT
481 TCACTTTCGT TTGTCTCACT ATGTCAAAAG AAGCTGAGTA CCATCCAGAA AGTgtaagtt
541 tttatttttt ggtaaaatag aaagtgttaag ttttataatt cattcaatty tttttgcctt
601 tcccttttcta tttattgcta taaatctaata accgcggtta aaatttgttt tgaaattaaa
15 661 cagTATGGAC CAGGAAGTCT GAAATCATAC Cgtaagtaaa aacttcttct tcttttatga
721 atcttgtttc ttattatata tcaaataaaa actcgattat catgattgca gAATGTGGAG
781 GACAATGCAC AAGGAGATGT AGCAACACAA AGTATCATAA GCCATGCATG TTCTTCTGCC
841 AAAAGTGTG TGCTAAATGC CTTTGTGTCC CTCCAGGCAC GTACGGCAAC AAACAAGTGT
901 GTCCTTGTTA CAACAACTGG AAGACTCAAC AAGGTGGACC AAAATGTCCA TAAacaaaaa
20 961 cattgagaga gaaaccccaa tctgtttcct attttattta attatttcca gtagctttt
1021 gttgtcgtga tggttaaatt atagtgtttt tgcaggtatc atttatcatc gataaacaat
1081 atcatataaa atcttctatg tttctttcac gttttgtttc ttttggtgta gtcaatacac
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1201 ctttcgtata gttaaaattc caaggattac ttttgattcg tttgggacaa tctattttat
25 1261 attttacttt ctaagtttgt ataactatat cttaaaagtg ttagacagag tcctaattgat
1321 tttagtataa ttgttactat ttagttaacgc ttcgaaaatt tggaaacttt ccaaagtgg
1381 ctatatcaat ttgattcaat aatctgcgct tccttctagt tttttacaat tatggagatt
1441 tttcgacgat gat

30

MAKLITSFLLLTILETFVCLTMS

KEAEYHPESYGPGLKSYQ

35

CGGQCTRRCSNTKYHKPCMFFCQKCCAKCLCVPPGTYGNKQVPCYNNWKTQGGPKCP *

c. At1g75750

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61 aacacacata aataatatgc tgataacaat gtcttaaaaa tctatttacc atttctagta
121 atcaatatct attgcaaaaa atatttataa gaatacaaat gaaaaatgat aaaatacaaa
181 tgattttctca attacctaaa aaatataaaa atgtcttact ttattttcag ccactgttgg
241 aaagtacttg caatcatatc gtattttgaa ttataaaact cagaaacaat tattttccct
301 gaaaagttaa aacttttaaat aagatatatta taaaaataaaa agaatagtct agaccgaaaa
10 361 tggggtcggt tgtccatcca aaggagtgtc ataaatagaa ccctccaagt tctcattagg
421 acacaacaac taaaaccaca tttatcatta cagtctgatt tgagctaagt tctctcatca
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541 CTCTTCTTGT TCTCCAAC TC CAGGCTG ATGTCgtacg tctttttcat cacaactaa
601 ttatactcaa tataatactt atgttttcaa aaacatattt ctcacatgtt acaacaatat
15 661 tcttgagGA AACTCACAG AAGAAAAATG GTTACGCAA GAAGATCGgt aattatatga
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841 CTGTGTCACA GAGCGTCCG GACTTGCTGC TACAGGTGCA ACTGTGTGCC TCCGGGTACG
901 TACGGAAACT ACGACAAGTG CCAGTGCTAC GCTAGCCTCA CCACCCACGG TGGACGCCGC
20 961 AAGTGCCCAT AAgagaaac aaagctctta attgctgagg ataatgggac gatgtcgttt
1021 tgttagtatt tactttggcg tatatatgtg gatcgaataa taaacgagaa cgtacgttgt
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1321 tgataactac tagactagct gagtataaga atattgatgt atatatattgc ggacaatttt
1381 gaatttatta taccattatt taatcacgac catataaaaa taattcctgt ttgcgttata
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30

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35

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D. At2g14900

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241 ttttcatgaa ttctaaatgt aaagtcttta taatcttatg ttacttttta caaatgttaa
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10 361 aagttgataa aacataatgg aaggaataat actgcagttc tattaataac taaagaagtt
421 ggtagattgg cctataaaag gagaaataag agaccacaag aaggtctatt attcggggac
481 taaagaaagc caaagaaaac ATGAAATAA TAGTCTCCAT CTAGTGTTA GCCTCTCTC
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1201 ATCGGTGTTT GAAGTATTGT GGGATATGTT GCAAAGACTG TCAGTGTGTT CCTCAGGCA
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1321 CTAATGTCC TTGAttctat ttctttccaa ccaaaaattt aaataaatga ataagagaga
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1441 ttctattttt acgaatttgt cttggtcttt ttgaagtaag tttttaataa ttgaaaagtg
30 1501 ctaaaattat gtggaaatcg ataagttaa tgaatgatat aatatataag tcctcagttt
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1741 gagaagaacg tgtttggtta aataattatg atggagttga gacaactttt aagagatttt
35 1801 aaaaagactg actaacgtgt taggttcacg acgt

MKIIVSILVLASLLLISSSLASATIS**DAFGSGAVAPAPQSKDGPALKW**

40

CGQKCEGRCKEAGMKDRCLKYCGICCKDCQCVPSGTYGNKHECACYRDKLSSKGTPKCP*

E. At2g18420

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181 tattatataat ttaatttagg aaatgaatgt taaatccttt aaattgtttt gatttcacaa
241 aaggataaag aaatattgggt tacatacatc ttaatgtgtt gaccaaaaca aataaaatgt
10 301 gataagaaac aataaaaacca ttttgaccaa agttcttata gttttaatat tctttaattg
361 tcatttggtta gtgactaata atattacatt aaacctaata tataaataga agcccatct
421 tctacgcctt tataatttagc aacaacaaaa aacattcatt tgtcattttg tctcctcttt
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35 **MAVFRVLLASLLISLLVLDFVHA**

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40

F. At2g30810

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10 361 atcctgaaat atatcataag aaaatcaaaa gtgaaataag agatcaaaaAT GATGAAGCTC
421 ATAGTTGTCT TTGTATATC CAGTTGTGTG TTTGCTACTC AATTTCTAA Tgtaaaaatt
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15 661 aatatcaatg ttatttttca aactacataa tttttaaata ttttattgat aacacaaatg
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1441 ttgaatttat ttaggccatg ttttaaaatc gtgtttggtt agattgaccc atgaaatggt
30 1501 gacatatttt aacattccta aatatgacta aaaatgatta aagatattta ataatatatt
1561 tgctctatta aaaatgatta aataaataat aata

MMKLIVVFVISSLLEATQFSNG

35

DELESQAQAPAIHKNGGEGSLKPEE**CPKACEYRCSATSHRKPCLEFFCNKCCNKCLCVPSGTYGHKEECPCYNNWTTKEGGPKCP***

40

G. At2g39540

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301 ctgtatgtta atatttttaa ctgaaaatag taccgacata acaagtaaag atatctttat
10 361 ttaaagtaac aaacattaat ttcacttcaa attctcacta ttaaggattc ctctctttgt
421 agccacattt caccatcact actttgtttt cgcatacttt taaattttgt atacgtagca
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541 TCCTCACATC TTCATTTTCT GTACTTTCAA GTGCTGATTC GTgtaagttt ttacttaatc
601 tagttaataa ttgtaggtca tgcattgtatc attttgaac aagttttctg aaattctaaag
15 661 atttttacata tatatgtgat aaatgaatta gcagCATGCG GTGGAAAGTG CAATGTGAGA
721 TGCTCAAAGG CAGGACAACA TGAAGAATGC CTCAAGTACT GCAATATATG TTGCCAGAAG
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10 961 tatataaaat aaaatcaatg cccccaatgt tggaaatctt caatgtgata tcttaataa
1021 tatcacgaat aaaaaagttt aaattttctca atctcatttt taatctttta tctaattttt
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1261 ttttgagaga ttcgttgact cactaccgga gaacgacgct atgtcagaga ccgccgtgtc
25 1321 aatcgattcg gaccgatcta agtcggagga agaagacyaa gaagagtatt ctccac

MKLVVVQFFIISLLLTSSFSVLSSA**DSS****CGGKCNVRC SKAGQHEECLKYCNICCCQKNCVPSGTFGHKDECP CYRDMKNSKGGSKCP***

35

H. At3g02885 (GASA5)

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61 cctaaactcg cttattttcc cttttctata tacagatatt atcatttagt acattttcat
121 ttcccaaaaca gagcgtttag acactagtca actacacaat ataattttcc aattttcact
181 gagagaaatg tttttttttt ttttttccaa ggcaagattt tagtcttttg gttctctata
241 cytgggtaat tagtgatttag taatttacac tgytgagtct ttgacattgt ctaagagaca
10 301 aaaacgacaa ggtggttag taattagaaa ttaaaatgac ctacttcccc agaatacacg
361 catgaacatt ggcaatacca aatttcttga ataccattga aggaaatcca cactaatcat
421 tttctctata aatatcttta atccgtttta ttgtttctta agaatacttc attggcaatc
481 aagatttttt aacccaaaaa ATGGCGAATT GTATCAGAAG AAATGCTCTT TTCTTCTTGA
541 CTCTTCTCTT TTTATTGTCA GTCTCCAACC TCGTTCAGgt aaaccactca aaacagattc
15 601 agttttattaa agtctgatat tgaagtttta tatattacag gctgctcgtg gaggtaaaaa
661 tgaccaaagg ctatacatto cttaaaaaatt taatggctat tagttttctg atattgaagt
721 tttatatata tatgacagGC TGCTCGTGGT GGTGGCAAAC TCAAACCCCA ACgtacggac
781 tcaaaaacttt tgytggttca tatgatcata ttaatttatt aatcactaat tattgataat
841 gttgataaat aaacttttaa gtaacaataa tgggtgttat tttgtgaaat gtcagttttc
20 901 tagtatactg tatgctgtga attataagca tgaacataaa gatctcaatg atttggtttt
961 tgyttgtttg ttgtgatatg cttttttgat ggaaacttca attgttagAGT GCAACTCAAA
1021 GTGTAGCTTC CGTTGTTTCAG CAACATCACA CAAGAAGCCA TGCATGTTCT TTTGCCTCAA
1081 GTGTTGCAAA AAATGTCTTT GTGTTCTCTC TGGCACTTTC GGCAACAAAC AAATGTGTCC
1141 ATGTTACAAC AACTGGAAGA CTAAAGAAGG CCGTCCAAAA TGTCTTAAa acttcttttt
25 1201 agatatattt gataatattc atctagtttt ggattatcaa acacttacta ctctgtttta
1261 atctgtttct acaagttggc gatttgtctc tacacttttt ttgtgtcttt tgctcttaac
1321 tgyttgtgtt gttatacgtg taagcccgcc caatgtgtca tggccgaact tattatggtt
1381 acatatattt gaaatgggct tcattatcaa ttgatttgag cctacaaaaa tgtagccata
1441 aagcccatat agttgtaatt gttaatattt cagtcataaa tatgattttc tatatctatg
30 1501 atttatctct agtggtgatg atgtttgtat gtggaagtca tgytctattt gcttccacgg
1561 tttaaaaacc atcaacttgc taaggtcaaa ttctaataat actgtgaaaa acattattta
1621 cgtgcgtaat tatatgaatt tatgaatagg ttttaattcc attttttctt aatagtgttt
1681 tatgtcaaa

35

MANCIRRNALFFLTLLFLLSVSNLVQAA40 **RGGGKLKPQQ****CNSKCSFRCSATSHKKPCMFCLKCKKCLCVPPGTFGNKQTCPCYNNWKTKEGRPKCP***

45

I. At4g09600 (GASA3)

5 1 taggctggca atttaactct gagacgtctt tcttgtatag agaataaaac atacgcgtgt
61 aaaagaaaac gcgtgaatcg aatgatgagt gttaacgttc gatcgagatg ccaccaaatc
121 ttttcattaa aatgaattgt ggaggacata ccacttttaa cgaggtcatt tccactgggt
181 gacatgtgga ctctactttg ggtggcatgt tcatatcttt ccacatcacc atgtaaacgt
241 gaaaacaccc accacactca cttacatctc aaacacatgt cttcattatc gtacgtagct
301 ccaaaaaaa aaatgaaaac taggttttagt gattctattt cgcaatgtat aatatacaac
10 361 ttgtaaaaat aaaatatattg aataagcatt ataaataaac ccaaagagggt gttagattta
421 tatacttaat tgtagctact aaatagagaa tcagagagaa tagttttata tcttgcacga
481 aactgcatgc tttttgagac ATGGCAATCT TCCGAAGTAC ACTAGTTTA CTGCTGATCC
541 TCTTCTGCCT CACCACTTTT GAGgttcata acttttgtct ttacttctcc atgaatcatt
601 tgcttcgtct tatecttaat tcatatgtgt ttgatcaatg ataataattc atcattctct
15 661 tcagCTTCAT GTTCATGCTG CTGAAGATTC ACAAGTCGGT GAAGGCGTAG TGAAAAATTGg
721 tatgtaacgc taacatatat gtaaagtgtt atatctctgt ttatatatga tttttaaacg
781 gttaaaaact agtcatatgt gtataaatat atcatgtgaa gATTGCGGTG GGAGATGCAA
841 AGGTAGATGC AGCAAATCGT CGAGGCCAAA TCTGTGTTG AGAGCATGCA ACAGCTGTTG
901 TTACCGCTGC AACTGTGTGC CACCAGGCAC CGCCGGGAAC CACCACCTTT GTCCTTGCTA
20 961 CGCCTCCATT ACCACTCGTG GTGGCCGTCT CAAGTGCCCT TAAacatata cacatacaga
1021 tgtgtgtata tgtcttcgc gagcacacac gtacgtttat gttttaagga caatagtatg
1081 tatgagcagc tataaacaaa ccagaagtta atgggttcag ttgaactagt ataagttgta
1141 tgaactgtgc ttcttttgaa caaccacttt tgctgtaagt ttagcaaccc tatttaataa
1201 attagagatt acaaaaaaaa aaatgaaaaa tgtttaaaaa acgtggattt ttaaatttgg
25 1261 gattaaaaat taattttcat tttggttgat ttgtcaataa attagctaag ttttgtatac
1321 taggccgttt aagatatgct gttaaatttt tgataataga gttgccttag aagttcataa
1381 ctgtaaatat ctaacttcac ttcaatctca caaacacacg aatcaacttc agcactaaga
1441 atcgaattga ccagaactga aagaaaagtaa aagaaaagct gaatacagag aatttaacga
30 MAIFRSTLVLLLILFCLTTF
ELHVHAAEDSQVGEVVKID
35 CGGRCKGRCSKSSRPNLCLRACNSCCYRCNCVPPGTAGNHHLCPYASITTRGGRLKCP*

J. At4g09610 (GASA2)

5 1 ttaacagttt aacaccataa tgtaaactc ggtttagcat tttggtgtaa ttctacctct
61 ttaaccatac atactaaaga cgcagagaag ttcatatggt agttaatcgt aaatagctaa
121 acctttaatt ggggttaaca tattatttaa cacttaacat ttaactattg atctctcatt
181 ttttttttat taaccaaaat aaatttcatt tagaaccaaa cgtttcaaaa actcgtaatg
241 ttttctcatt aaatcttatt tatagctcac acaagaaaaa actacggaca tgcattgcacc
301 caattatata catggattat tatttttagt gttataatat gatacaaaat aaaaaacatt
10 361 tggatagcgc ataggcgata gccactataa atataccaaa gaggttggat tatacatata
421 gccgtaatac caaagagagt atcagataga aatagttcta atattttgta caactcacag
481 aaattgcatg agtttcgaac ATGGCAGTCT TCCGAAGTAC ACTGGTCTG TTACTAATCA
541 TCGTCTGTCT CACCACTTAT GAGgtttata atatttttg tctttatagt tccccaagaa
601 caccatagcaa tattatactc aattcatggt tatatgataa tgactgatca ttctcttcag
15 661 CTTACGCTCC ACGCTGCTGA TGGTGCAAAG GTCGGTGAAG GCGTAGTGAA AATCGgtatg
721 taaccctaac ttatatataa cacgttggtt tataacttaa tatttctgat ggggtgcactc
781 tcttcccaac ttatatatat ctttgttatg gagaatgtct caagctttta atgagatggt
841 atatctcgga gaaggaaact atgaactaaa agctttggat tcctttgcaa caaatataaaa
901 cttttgatgg gtttaaaccg attaaattag ttacatgtgt ttgatgaatg tatgtatgat
20 961 tgtagATTGT GGTGGGAGAT GCAAAGATAG ATGCAGCAA TCTTCGAGAA CGAAGCTATG
1021 CTTGAGAGCG TGCAACAGCT GTTGTCCCG CTGCAACTGT GTGCCACCTG GTACTTCTGG
1081 AAACACCCAC CTTGTCTCTT GCTACGCCTC CATTACCACT CACGGTGCC GCCTCAAGTG
1141 CCCTTAAaat ttcttctgtg tctgtttctg tttctacttc tatttcgaat atatgtacat
1201 gtgtgtgtac gtgtgtatgt atacaagtac tgctatgttt tggaggacaa aagtatatgt
25 1261 atgagaagct ataaactaat tagaagttga tggttatgctg tattatcaaa ccgtgttact
1321 tctgaacaac caatttcggt ttgttccaag tttggcaacc ctaaaataaa aattcaaaat
1381 gattggagac tactcgttaa tagacattga aaacgatgaa atctcgttac gtttttatat
1441 tttttgaact gtaatatatt tatgcagaag cggttttgta atgggccgac aaaaaaaaaaag
1501 tggttttgta atggatatga ttccgatcta ttctggaaat ggtctcaaaa agtagagttg
30 1561 agatctcaat acgaaaatga accctttcgt ttgatttatc aaagcctttt attttgaaaa
1621 cgttaaattc tcactaggat ctctctt

35 MAVFRSTLVLLIIVCLTTY

ELHVHAADGAKVGEVVKID

CGGRCKDRCSKSSRTKLCLRACNSCCSRCNCVPPGTSGNTHLCPCYASITTHGGRLKCP**

40

K. At5g15230 (GASA4)

5 1 aaatattcac cctaaaaatga atctaaaaat gtacaaaaat acaggaaaat aaaactaagc
61 agaaatgtcc taagaaaact aaagttttta aaaaataatc ttcaaagaga tactccaact
121 ggtggttataa gcaaaacttg atttatcaaa aacaggttca tagtatttta tatttagtac
181 tataagcttt ccttaaacca tgtgcaaaac catctaccgc agtctaatta ccaatagcaa
241 gtaataaaat gggactaaca ttggaggcat acgtggaata atataattgg aggaatacag
10. 301 taataatgat atgtgttgcc acaggggaata attgatacga gcaaattggt gtatatatag
361 cttatatgca acatcattgg gtccctcaacc aaaaactcct ctctcagtac acttcttttc
421 atacctcaag agactaaaaac tagtttgagg agatttagag gagtgtttgg ttctttggat
481 aacaatatcc caaactgaaa ATGGCTAAGT CATATGGAGC TATCTTCCTC TGGACCTCA
541 TTGTCCTCTT CATGCTTCAA ACCATGgtaa cacctctatt attttttct tctttcaatg
601 tttgaaaata ttgaagataa tatatttgat tgttttcctt attgacgaac gatatgagac
15 661 aaatgtgggt tctattatg tacttttagt tggaatata ttaatttagc ctttttaatg
721 aaattaattt tacttgtttt tctctctctt ttttttcgtt ttttagGTTA TGGCCTCAAG
781 TGGATCTAAT GTGAAGTGGG GCCAGgtcag ttttattatt gaatcgacta gtaattacct
841 ttttaactat attttatacc tattgttatc tcgtaactta acgaaaagtg attaatagat
20 901 tacctttttt ggttaatttt cagAAACGTT ATGGACCAGG AAGCCTGAAA CGTACCgta
961 agttttttct tcacagctat tcttaaacaa ttttttttta atctcataat cgacgaaaaa
1021 taacaattc aagaaatctt ttattgtgtt ataataaaaa aaaaataagca tttcagttgc
1081 agaaaataag ttgaaagtga agtgtaagt ggactgtttg gtcagatccg tagactcaaa
1141 atatattaga tattgacgaa attgcccctt aatatggtca tacagtcaaa gcaaccact
1201 atcttgagac ccacaaaaa gtaaaaaaaa aagctaata atttccacta gattctgttg
25 1261 tttttattag taataaaaaa tttttgagtg ttaacatttt gatattgttt gattttgaaa
1321 caaccagAAT GCCCATCGGA ATGTGATAGG AGGTGTAAAA AGACACAGTA CCACAAGGCT
1381 TGCATTACGT TCTGCAACAA ATGCTGCAGG AAGTGTCTCT GTGTGCCTCC GGGTTACTAT
1441 GGGAAACAAAC AAGTTTGCTC CTGCTACAAC AACTGGAAAA CTCAAGAGGG TGGACCAAAA
1501 TGCCCTTGAA aaaaatctccc ttctgtccct tttataata aaaattttca actataacta
30 1561 aatttccttt gatcaatgtt ttatctactt tattcctaatt gttgtaagt tatgtcactc
1621 cttttcggat tttgttctaa atcctaaaaa aaatgagagt ggccctatga atgatatttt
1681 tcatgaatac ttgtgtttct aaagatatat tcccatcat ccacaaaaa aaaagatatt
1741 ttccatttcg aaaaatagtaa tactataaag ggtaaggcaa accaaataat acaatttaaa
1801 aaattcctgc gaaagaagta tgcataatga gaaaagagt acattgggtc tctcgcccca
35 1861 gtactaaaaa gccattatt gatttttcca agctttttac aaaatcacgt gttctaacgc
1921 gattgctttt tgccgcaatc ttcttttata caagacttgg gctttgggca gttggaaata
1981 aataacgaca acgatatttt acaatcgggt

MAKSYGAIFLLTLIVLEMLQTMV

40

MASSGSNVKWSQKRYGPGSLKRTQ**CPSECRRCKKTQYHKACITFCNKCCRKCLCVPPGYYGNKQVCSCYNNWKTQEGGPKCP****

45

L. At5g14920

1 ttgctcactg gtgcaataat cgaagtgaag agcctcttta tatgaaatat ataagcgaca
5 61 cagccttatg ggcaaatcga atgctatttta tttatttgat aagaagatta ataatttcaa
121 tttgtcatcc actagtctct tggggctactc aaaacatatac accaaaaagt ccatagagtt
181 atttgttctt atttactgat aaagtattcc aagttgatgt acgaataaag tggcaatttc
241 atgtattatc aatataatcc atttttggga atctgatatt ttgtttatcc tcgagctctg
301 agagatatat tttggtgcag tgaagggttca aagctggcat gcatgatgca tataataact
10 361 gctctggacc taatacttac tacgcattta aattaatatt tatggataat atggtttaata
421 aataaggaac ttctatttat atcacaaaag gtcactggtc ttcttcgtgt gacttcacca
481 ctttctcatc tccccaaaa ATGGCTCTCT CACTTCTTTC AGTCTTTATC TTTTTCATG
541 TCTTTACCAA Tgtaagttat tcttactttt cataacaaaa ggtgttatta tgttaaagac
601 tacataatag tatacaatta tgtgcattac gttttcgcgt attgtaacta actatgtatt
15 661 ttgattaatc accgagcagG TTGTTTTTGC TGCTTCAAT GAGGAATCCA ACGCCTTAgT
721 acgttttcta atttccagtt taattatttc tatgctgctt taactatata ctcaggcatt
781 tttatttgatt attgtgatg aagttaaatt ttggtatatg ttgtattaa atttatagGT
841 TTCTTTACCA ACGCCAACAC TTCCATCGCC ATCTCCGGCT ACCAAACCGC CGTCGCCAGC
901 TCTCAAACCG CCGACGCCGT CGTACAAGCC ACCCAGCTG CCAACTACTC CTATTAAACC
20 961 ACCCACCACA AAACCTCCGG TCAAACCTCC AACTATTCCG GTTACACCAG TAAAACCTCC
1021 GGTTCACACT CCTCGATCA AACTACCGCC GGTACAACCA CCTACGTACA AACCCCAAC
1081 GCCAACAGTT AAACCACCGT CCGTCCAACC ACCTACGTAC AAACCCCAAC CTCCAACGCT
1141 TAAACCACCC ACTACATCAC CGGTAAACCC ACCCACTACG CCACCAGTTC AATCACCGCC
1201 GGTCCAACCA CCTACGTACA AACCCCAAC GTCACCGGTT AAACCACCCA CCACAACCTCC
25 1261 ACCGGTTAAA CCCCCACCA CGACGCCACC GGTCCAACCA CCTACGTACA ATCCCCAAC
1321 TACACCGGTT AAACCACCTA CAGCGCCGCC TGTCAAACCT CCAACACCAC CTCCCGTAAG
1381 AACTCGGATA Ggtaataata attttctttc aaaagtgtga tgattatcgg tcggttgatta
1441 gatcggatgt ataattggac taaatttttg acggtttagA TTGCGTGCCT TTATGTGGA
1501 CGAGGTGTGG GCAACACTCG AGGAAGAAGC TATGTATGAG AGCGTGCCTC ACGTGTCTGT
30 1561 ACCGCTGCAA GTGTGTTCCT CCAGGCACCT ACGGTAATAA GGAGAAGTGT GGATCTTGTT
1621 ACGCCAACAT GAAGACACGT GGTGGAATAA CCAATGTCC TTGAaccttt atatgacgat
1681 gggttgtaaa cgaataaatt taaatcaatg gagtttttat aagtttgtaa tgcgtttgtt
1741 tttgttatag taatattgag ttggatcttt gtttacggga cgtagaatac taaataatga
1801 aaaaaacott ctcgatgaat taagggtttt atgaatttgt ttgtattga ataatatagg
35 1861 gatggataaa gttttattat tctaacaggt tactttatta ggcatttctt cggctcatgt
1921 aactcttgta tcgctgaaac tatgtaatag atagaagaac ctaaaaaaag aaagaaaaca
1981 agaaatgcac atagcgaagc tcaaaagatg agtggtctgc tagcggtaat gttgttatct
2041 agttgggtca aatgctctaa ttgcaaatct tatttgggcc ttatatagac tcttatgtgc
40 2101 atatggtcca gcctatttgg gccgatgtgt ttgaagatca tttgggaaag tcttgcgcaa
2161 ggag

MALSLLSVFIFFHVFTNVVFAAS

45 NEESNALVSLPTPTLPSPSPA
TKPPSPALKPPTPSYKPPTLP
TTPIKPPTTKPPVKPPTIPVT
PVKPPVSTPPIKLPPVQPPY
KPPPTPTVKPPSVQPPYKPPT
50 PTVKPPPTSPVKPPTTPFVQS
PFVQPPPTYKPPTSPVKPPTTT
PFVKPPTTTTTPFVQPPTYNPPT
TFVKPPTAPFVKPPTPPFVRT
RID

55

CVPLCGTRCGQHSRKNVCMRACVTCCYRCKCVPPGTYGNKEKCGSCYANMKTRGGKSKCP*

M. At5g59845

5 1 gacttgagta tgaatccaat aaccacaaat ttatgcagat tttagaatac ttcttataaa
61 tctttaaata gaataacaac
121 agattctaca tgacatttta aatcactaaa actcttttga aatcataaac caataacaac
181 cccttagttt ttactatttt gaattctgac gtactttttt attagttaa tttctataaa
241 tgagaaaaca ttaattattt cttaatcttt gaacttaagc cccacaaaaa tcttataaat
301 tgggacagat ggactagata acaagcgttt cacctactcc aaaatttccc tataagtaac
10 361 tcttttttga acctcctttt ctteccaaac catcactcct tttgcattgt gtgaaacctt
421 cgagttttct cttcatcttc tcaaagtaac aaactttctc caaacagatt attattaaaa
481 caatctcatc aagaactacg ATGAAATTC CGGCTGTAAA AGTTCTTATT ATCTCTCTTC
541 TCATCACATC TTCTTTGTTC ATACTCTCAA CCGCGGATTC GTgtaagtat acacaatgca
601 ttttcttatt ttagatactt ttctcattag aaatttagct ttcttaataa aattgtattg
15 661 tgatgatgga ttaatttagCA CCATGCGGAG GAAAATGCAA CGTGAGATGT TCAAAGGCAG
721 GAAGACAAGA TAGGTGTCTC AAGTATTGTA ATATATGTTG CGAGAAGTGT AACTATTGTG
781 TTCCTTCAGG CACTTATGGA AACAAAGATG AATGCCCTTG TTACCGCGAT ATGAAGAACT
841 CCAAAGGCAC GTCCAAATGT CCTTGATcat gttcttaaga ttatccttat agacacaata
901 tcttgaaatg ttaagattgt gcttgatgcc taaaataatg agcttgagat acttctatga
20 961 atgaatatgt gaaagatttt gacaataaaa tgatttgatg tattaataa ttcttagtga
1021 agttatatat gtataaatga agtatgaaat atacattgta tgttgcttta catgagaaag
1081 ataaatctac aacaatccaa tgtatgaaaa ttttactaag ttaactgatc agaaacgtta
1141 attatggttt agaattctgt ggagagatga ttacttttgt aagagaaatt gattgtttgt
1201 tgtcaatgag gataaagtaa gaagccattt ctcaacacat ggacttgata gcaaaactaaa
25 1261 caaggctcaa gcattgaaat tgaaacgtct cgatagataa gattggctca agaaaagcaa
1321 gtgttttttg ttgtagaaaa cagaaattga aattactgtc tacttt

30 MKFPAVKVLIISILLITSSLFILSTA

DSSP

CGGKCNVRC SKAGRQDRCLKYCNICCEKCNVCP SGTYGNKDECPYRDMKNSKGT SKCP*

35

N. At3g10170

genomic structure before splicing and processing 5'- towards 3'
predicted orf sequences are underlined

5

CTGTTTTCAGAAAATGGCAACAAACTTAGCATCATTGTTTTCTCCATTG
TTGTGTTACATCTTCTTCTGTCTGCCATATGCATGTAAGTGTTTCAACA
CTCTATTCTCTCTATGTTTCACATTTATCAACTTTATCTTATACGTCCCTGA
ATAAAACACAGCCTATATACTTGGAACTCTCTGCTCGACAACCACAACCA
CCACAGTCGCAACCACAACCTGCCGCATCACAATAACTCTCAAGTGAGTTT
CTCGGTTTCATCACTACTCAAAAAAAGAGTTTCATCGAATCTACAAAACCT
TTTTAACATCCTTTGCATCTTCTTGTGATTTTGGCAGTACGGTACTACT
CAAGGCAGTCTTCAACCCCAAGGTAAACCCACTGACTAGCCTAGTTTTTA
ATTAATGTTTGTGCTGAATGCGAACTAAATCCGCTATTCCACCTTTATT
AGAGTGCGGGCCAAGGTGTGGAGATAGATGCTCGAATACACAATACAAGA
AGCCGTGTTTGTCTTCTGCAACAAATGTTGTAACAAGTGCTTGTGTGTG
CCCCCAGTACTTATGGCAATAAGCAAGTATGTCCTTGCTATAACAACCTG
GAAGACCAAGAGCGGTGGACCAAAATGCCCTTAGTTTCTCCTCTTAATTA
CTTTAGCATAACTCCATGTAATTTGTTAATCTACCTATCATAATTTATA
TATGTATTGGACTCTTCCATAATCACATCAGTTCTCTGTGATTATGACGT

10

15

20

Amino acid sequence of the predicted pre-pro-peptide
the first line represents the signal sequence
the second (set of) lines represents the the pro-peptide
the last line represents the conserved Cysteine motif.

25

MATKLSIIVFSIVVLHLLLSAHMH

FLINVCAECETKSAIPPLLE

30

CGPRCGDRCSNTQYKKPCLEFFCNKCCNKCLCVPPGTYGNKQVPCYNNWTKSGGPKCP*

35

They consist of an N-terminal signal peptide, followed by a variable domain (involved in mobility or cell wall attachment) and a C-terminal domain with 12 conserved cystein residues.

The consensus of this last domain is:

C-C-RC-----C---C--CC-(R/K)C-CVP(P/S)GT-G(N/H)---C-CY-----G--KCP*

(-) = any amino acid;

(C) = conserved C-residue

(/) = either one or the other amino acid at this position;

* = stopcodon

Some members of this gene family have been described previously, and represent the GASA family in *Arabidopsis thaliana* (Plant Mol. Biol. 36 (1998). Similar family members containing the same structural motifs are present in rice (like GASR1) and tomato (Plant Journal 2 (1992) 153-159; Mol. Gen. Genet. 243 (1994) Taylor and Scheuring). In *Arabidopsis*, the GASA gene family represents 14 different membres, similar as the number for the RKS gene family. Our data on the similar phenotypes for RKS4 and GASA3 (figure 6) and the fact that there are similar numbers of ligands and receptors suggest that there is a single GASA ligand molecule interaction with a single RKS molecule. T-DNA knock out phenotypes observed with several of the other GASA peptide ligand genes also show modifications of organ and plant size like the appearance of extreme dwarf plants resembling brassinosteroid insensitive mutants. Co-localization of RKS genes and GASA ligands on the genome (see figure 4) could provide clues of molecular interactions between GASA molecules and RKS molecules (similar as for S locus proteins and S locus receptor kinases).

Furthermore, in the chapter discussing the effects of roots in RKS transgenic plants, it was shown that overexpression of RKS genes can result in the formation of lateral roots (figure 26). One of the GASA ligands is involved in the formation and/or outgrowth of lateral roots as discussed in Mol. Gen. Genet. 243, 1994, 148-157.

Intracellularly, this signal is transmitted onto membrane (but not necessarily plasma membrane) associated NDR-NHL proteins. At least some of the functions of the syntaxin-like NDR-NHL proteins would thereby result in the regulation of vesicle transport and /or the positioning of new cell wall formation. Neighboring cells are known to influence and determine the developmental state and the differentiation of cells. In transgenic plants with RKS and / or NDR-NHL expression cassettes the positioning of new cell walls is modified, resulting in abnormal neighboring cells, resulting in abnormal development of groups of cells like flower meristem primordia as observed and shown with RKS0, RKS13 and NHL10.

Table 2 overview of accessions numbers of RKS signal complex genes in *arabidopsis* and in rice:

Gene code	contig	gene prediction in At database	<i>Oryza sativa</i> japonica contig	approximate position in bp around:
5	RKS0 At1g71830 f14o23	ok	OSJNBa0036B21	52.000
	RKS1 At1g60800 f8a5	ok	P0038C05	60.000
	RKS2 At5g65240 mqn23	ok	OJ1212_C08	8000
	RKS3 At5g63710 mbk5	ok	see rks2	
10	RKS4 At2g23950 t29e15	wrong, exon missing	P0708B04	35.000
	RKS5 At5g45780 mra19	wrong, exon missing	OJ1077_A12	102.000
	RKS6 At5g10290 wt e 23	ok	see rks2	
	RKS7 At5g16000 ku e 24	ok	P0038C05	60.000
	RKS8 At1g34210 f23m19	ok	OJ1134_B10	90.000 & 1000 2
15	different genes!			
	RKS10 At4g33430 en d 25	wrong, exon missing	see rks0	
	RKS11 At4g30520 wu d 20	wrong, exon missing	see rks4	
	RKS12 At2g13800 f13j11	wrong, exon missing	see rks10	
	RKS13 At2g13790 f13j11	ok	P0633E08	36.000
20	RKS14 At3g25560 mw12	wrong, exon missing	OSJNBb0015G09	36.000
	ELS1 At5g21090 ch e 52	ok	P0003H10	53.000
	ELS2 possibly allelic variant of ELS1 no genomic sequence identified yet			see els1
	ELS3 At3g43740 by c 21	ok	P0468B07	52.000

25

Homology between aa sequences from *arabidopsis* proteins are compared with the rice databases using:
http://mips.gsf.de/proj/thal/db/search/search_frame.html
 protein sequences based on *Oryza sativa* japonica contig sequences.

30

Arabidopsis thaliana ELS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

```
ttactctcaaattccttttcgatttcctctcttaaacctccgaaagctcac
ATGGCGTCTCGAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAACCCTAA
CCTTAGCTTTGATTCACCTGGTCGAAGCAAACTCCGAAGGAGATGCTCTCTA
CGCTCTTCGCCGAGTTTGACAGATCCAGACCATGTCCTCCAGAGCTGGGAT
CCAACTCTTGTTAATCCTTGTACCTGGTTCCATGTCACCTGTAACCAAGACA
ACCGCGTCACTCGTGTGGATTGGGAAATTCAAACCTCTCTGGACATCTTGC
GCCTGAGCTTGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAAAAC
AACATCCAAGGAACTATACCTTCCGAACTTGGAAATCTGAAGAATCTCATCA
GCTTGGATCTGTACAACAACAATCTTACAGGGATAGTTCCCACTTCTTTGGG
AAAATTGAAGTCTCTGGTCTTTTTACGGCTTAATGACAACCGATTGACGGTC
CAATCCCTAGAGCACTCACGGCAATCCCAAGCCTTTAAAGTTGTGACGTCTC
AAGCAATGATTTGTGTGGACAATCCCAACACGGACCCTTTGCTCACATTCC
TTTACAGAACTTTGAGAACAACCCGAGATTGGAGGGACCGGAATTACTCGGT
CTTGCAAGCTACGACACTAACTGCACCTGAacaactggcaaacctgaaaat
gaagaattggggggtgaccttgtaagaacacttcaccactttatcaaatatc
acatctactatgtaataagtatatatatgtagtccaaaaaaaaaaaaaaaaaa
```

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich

repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

5

MASRNYRWELFAASL
TLTLALIHLEVEANSEG

DALYALRRSLTDP

10

DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

DLGNSNLSGHLA

15

P ELGKLEHLQYLELYKNNIQGTI
PSELGNLKNLISLDLYNNNLTGIV
PTSLGKLKSLVFLRLNDNRLTGPI
PRALTAIPSLKVVDVSSNDLCGTI
PTNGPFAHIPLQNFENNPRLEGPE

20

LLGLASYDTNCT

Arabidopsis thaliana ELS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 aaaattactcaaattcctattagattactctcttcgacctccgatatgctcac
ATGGCGTCTCGAAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAATCCTAA
CCTTAGCTTTGATTACCTGGTCTGAAGCAAACCTCCGAAGGAGATGCTCTTTA
CGCTCTTCGCCGGAGTTTAACAGATCCGGACCATGTCCTCCAGAGCTGGGAT
CCAACCTCTTGTTAATCCTTGTACCTGGTTCCATGTCACCTGTAACCAAGACA
15 ACCGCGTCACTCGTGTGGATTGGGGAATTCAAACCTCTCTGGACATCTTGC
GCCTGAGCTTGGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAAAAC
AACATCCAAGGAAGTATACCTTCCGAACCTGGAAATCTGAAGAATCTCATCA
GCTTGGATCTGTACAACAACAATCTTACAGGGATAGTTCCCACTTCTTTGGG
AAAATTGAAGTCTCTGGTCTTTTTACGGCTTAATGACAACCGATTGACGGGG
20 CAATCCCTAGAGCACTCACTGCCAATCCCAAGCCTTAAAAGTTGTGGATGTC
TAAGCAATGATTTGTGTGGAACAATCCCAACAAACGGACCTTTTGCTCACAT
TCCTTTACAGAACTTTGAGAACAAACCCGAGGTGGAGGGACCGGAATTACTC
GGTCTTGCAAGCTACGACACTAACTGCACCTGAagaaattggcaaaacctga
aaatgaagaattgggggggaccttgaagaacacttcaccactttatcaa
25 atcacatctactatgtaataagtatatatatgtagtccaaaaaaaaaatgaa
gaatcgaatagtaatatcatctggtctcaattgagaactttgaggtctgtgt
atgaaaattaaagattgtactgtaatgttcggttggtggattctgagaagta
acatttgtattgggtatggtatcaagttgttctgccttgtctgcaaaaaaaaa

30

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS2 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as
35 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain

contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be
5 involved in attachment to other proteins or structures within the cell wall.

MASRNYRWELFAASL
ILTLALIHLEVEANSEG

10

DALYALRRSLTDP
DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

15

DLGNSNLSGHLA

P ELGKLEHLQYLQLYKNNIQGTI
PSELGNLKNLISLDLYNNNLTGIV
PTSLGKLKSLVFLRLNDNRLTGPI
20 PRALTAIPSLKVVDVSSNDLCGTI
PTNGPFAHIPLQNFENNPRLEGPE

LLGLASYDTNCT

25

Arabidopsis thaliana ELS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttctctctccggcgaaaacc**ATGGTGGCGCAAAACAGTCGGCGGGAGCTTCTAGCAGCTT**
CCCTGATCCTAACTTTAGCTCTAATTCGTCTAACGGAAGCAAACCTCCGAAGGGGACGCTC
TTCACGCGCTTCGCCGGAGCTTATCAGATCCAGACAATGTTGTTTCAGAGTTGGGATCCAA
CTCTTGTTAATCCTTGTACTTGGTTTCATGTCACTTGTAATCAACACCATCAAGTCACTC
GTCTGGATTTGGGGAATTCAAACCTATCTGGACATCTAGTACCTGAACTTGGGAAGCTTG
15 AACATTTACAATATCTTGAACCTCTACAAAAACGAGATTCAAGGAACTATACCTTCTGAGC
TTGGAAATCTGAAGAGTCTAATCAGTTTGGATCTGTACAACAACAATCTCACCGGGAAAA
TCCCATCTTCTTTGGGAAAATTGAAGCGGCTTAACGAAAACCGATTGACCGGTCCTATTC
CTAGAGAACTCACAGTTATTTCAAGCCTTAAAGTTGTTGATGTCTCAGGGAATGATTTGT
GTGGAACAATTCAGTAGAAGGACCTTTTGAACACATTCCTATGCAAACTTTGAGAACA
20 ACCTGAGATTGGAGGGACCAGAACTACTAGGTCTTGCGAGCTATGACACCAATTGCACTT
AAaaagaagttgaagaa

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS3 protein.

25 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a
30 leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each
35 approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

MVAQNSRRELLAASL
ILTLALIRLTEANSEG

5 DALHALRRSLSDP
DNVVQSWDPTLVN

PCTWFHVTCNQHHQVTRL

DLGNSNLSGHLV

10 P ELGKLEHLQYLELYKNEIQGTI
PSELGNLKSLSLDLYNNNLTKGI
P SSLGKCLKRLNENRLTGPI
PRELTVISSLKVVVDVSGNDLCGTI
PVEGPFHEHIPMQNFENNLRLLEGPE

15 LLGLASYDTNCT

Arabidopsis thaliana RKS0 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atttttattttattttttactctttgtttgttttaatgctaattgggtttttaaaagggtt
atcgaaaaaatgagtgagtttgtgttgaggttgtctctgtaaagtgttaatggtggtgat
tttcggaagttagggttttctcgatctgaagagatcaaataagattcgaaatttacca
ttgttgtttgaa**ATGGAGTCGAGTTATGTGGTGT**TTATCTTACTTTCAGTATCTTACTT
CCGAATCATTCAGTGTGGCTTGCTTCTGCTAATTTGGAAGGTGATGCTTTCATACTTTG
15 AGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAAGAGCTGGGATCCTACGCTAGTGAAT
CCTTGCACATGGTTCCATGTCACTTGCAACAACGAGAACAGTGTCAAGAGTTGATTTG
GGGAATGCAGAGTTATCTGGCCATTTAGTTCCAGAGCTTGGTGTGCTCAAGAATTTGCAG
TATTTGGAGCTTTACAGTAACAACATAACTGGCCCGATTCTAGTAATCTTGGAATCTG
ACAAACTTAGTGAGTTTGGATCTTTACTTAAACAGCTTCTCCGGTCTTATCCGGAATCA
20 TTGGGAAAGCTTTCAAAGCTGAGATTTCTCCGGCTTAACAACAACAGTCTCACTGGGTCA
ATTCTATGTCACTGACCAATATTACTACCCCTCAAGTGTTAGATCTATCAAATAACAGA
CTCTCTGGTTCACTTCCTGACAATGGCTCCTTCTCACTCTTCACACCCATCAGTTTTGCT
AATAAAGTTAGACCTATGTGGACCTGTTACAAGTCACCCATGTCTGGATCTCCCCCGTTT
TCTCTCCACCACCTTTTATTCAACCTCCCCAGTTTCCACCCCGAGTGGGTATGGTATA
25 ACTGGAGCAATAGCTGGTGGAGTTGCTGCAGGTGCTGCTTTGCCCTTTGCTGCTCCTGCA
ATAGCCTTTGCTTGGTGGCGACGAAGAAGCCCACTAGATATTTTCTTCGATGTCCCTGCC
GAAGAAGATCCAGAAGTTCATCTGGGACAGCTCAAGAGGTTTTCTTTGCGGGAGCTACAA
GTGGCGAGTGATGGGTTTAGTAACAAGAACATTTTGGGCAGAGGTGGGTTTGGGAAAGTC
TACAAGGGACGCTTGGCAGACGGAACCTTGTGTGCTGTCAAGAGACTGAAGGAAGAGCGA
30 ACTCCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCAGTTCAT
CGAAACCTGTTGAGATTACGAGGTTTCTGTATGACACCGACCGAGAGATTGCTTGTGTAT
CCTTACATGGCCAATGGAAGTGTGCTTCGTGTCTCAGAGAGAGGCCACCGTCACAACCT
CCGCTTGATTGGCCAACGCGGAAGAGAATCGCGCTAGGCTCAGCTCGAGGTTTGTCTTAC
CTACATGATCACTGCGATCCGAAGATCATTCACCGTGACGTAAAAGCAGCAAACATCCTC
35 TTAGACGAAGAATTCGAAGCGGTTGTTGGAGATTTTCGGGTTGGCAAAGCTTATGGACTAT
AAAGACACTCACGTGACAACAGCAGTCCGTGGCACCATCGGTCACATCGCTCCAGAATAT
CTCTCAACCGGAAAATCTTCAGAGAAAACCGACGTTTTCGGATACGGAATCATGCTTCTA
GAACTAATCACAGGACAAAGAGCTTTTCGATCTCGCTCGGCTAGCTAACGACGACGACGTC
ATGTTACTTACTGGGTGAAAGGATTGTTGAAGGAGAAGAAGCTAGAGATGTTAGTGGAT
40 CCAGATCTTCAAACAACTACGAGGAGAGAGAACTGGAACAAGTGATACAAGTGGCGTTG

CTATGCACGCAAGGATCACCAATGGAAAGACCAAAGATGTCTGAAGTTGTAAGGATGCTG
GAAGGAGATGGGCTTGCGGAGAAATGGGACGAATGGCAAAAAGTTGAGATTTTGAGGGAA
GAGATTGATTTGAGTCCTAATCCTAACTCTGATTGGATTCTTGATTCTACTTACAATTTG
CACGCCGTTGAGTTATCTGGTCCAAGGTAaaaaaaaaaaaaaaaaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS0 protein.

10 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MESSYVVFILLSLILLPNHSL
WLASANLEG

35

DALHTLRVTLVDP
NNVLQSWDPTLVN

PCTWFHVTCNNENSVIRV

DLGNAELSGHLV

40

P ELGVLKNLQYLELYSNNITGPI

PSNLGNLTNLVSLDLYLNSFSGPI
PESLGKLSKLRFLRLNNSLTGSI
PMSLTNITTLQVLDLSNNRLSGSV
PDNGSFSLFTPISFANNLDCGPV

5

TSHPCPGSPPFSPPPP
FIQPPPVSPTSGYGITG

AIAGGVAAGAAL

10 PFAAPAIAFAWW

RRRKPLDIFFDVPAEEDPE
VHLGQLKRESLRELQVAS

15 DGFSNKNILGRGGFGKVYKGRAD

GTLVAVKRLKEERTPGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPPSQPPLDWPTRKRIALGSA

20 RGLSYLHDHCDPKIIHRDVKAA

NILLDEEFEAVVGDFGLAKLMD
YKDTHTTAVRGTIGHIAPEYL
STGKSSEKTDVFGYGIMLLELI
TGQRAFDLARLANDDDVMLLDW

25 VKGLLKEKKLEMLVDPDLQTNV

EERELEQVIQVALLCTQGSPME
RPKMSEVVRMLE

GDGLAEKWDEWQKVEILREEIDLS

30

PNPNSDWILDSTYNLHAVELSGPR

Arabidopsis thaliana RKS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ccaaagttgattgctttaagaagggat**ATGGAAGGTGTGAGATT**TGTGGTGTGGAGATTA
GGATTTCTGGTTTTTGTATGGTTCCTTTGATATCTTCTGCTACACTTTCTCCTACTGGT
GTAAACTATGAAGTGACAGCTTTGGTTGCTGTGAAGAATGAATTGAATGATCCGTACAAA
GTTCTTGAGAATTGGGATGTGAATTCAGTTGATCCTTGTAGCTGGAGAATGGTTTCTTGC
ACTGATGGCTATGTCTCTTCACTGGATCTTCCTAGCCAAAGCTTGTCTGGTACATTGTCT
15 CCTAGAATCGGAAACCTCACCTATTTACAATCAGTGGTGTGCAAAACAATGCAATCACT
GGTCCAATTCCGGAAACGATTGGGAGGTTGGAGAAGCTTCAGTCACTTGATCTTTCGAAC
AATTCATTCAACGGGGAGATACCGGCCCTCACTTGGAGAACTCAAGAACTTGAATTACTTG
CGGTAAACAATAACAGTCTTATAGAACTTGCCCTGAGTCTCTATCCAAGATTGAGGGA
CTCACTCTAGTCGACATTTTCGTATAACAATCTTAGTGGTTCGCTGCCAAAAGTTTCTGCC
20 AGAACTTTCAAGGTAATTGGTAATGCGTTAATCTGTGGCCCCAAAAGCTGTTTCAAACGTGT
TCTGCTGTTCCCGAGCCTCTCACGCTTCCACAAGATGGTCCAGATGAATCAGGAACTCGT
ACCAATGGCCATCACGTTGCTCTTGCAATTTGCCGCAAGCTTCAGTGCAGCATTTTTTGT
TTCTTTACAAGCGGAATGTTTCTTTGGTGGAGATATCGCCGTAACAAGCAAATATTTTTT
GACGTTAATGAACAATATGATCCAGAAGTGAGTTTAGGGCACTTGAAGAGGTATACATTC
25 AAAGAGCTTAGATCTGCCACCAATCATTTCAACTCGAAGAACATTCTCGGAAGAGGCGGA
TACGGGATTGTGTACAAAGGACACTTAAACGATGGAACCTTGGTGGCTGTCAAACGTCTC
AAGGACTGTAACATTGCGGGTGGAGAAGTCCAGTTTCAGACAGAAGTAGAGACTATAAGT
TTGGCTCTTCATCGCAATCTCCTCCGGCTCCGCGGTTTCTGTAGTAGCAACCAGGAGAGA
ATTTTAGTCTACCTTACATGCCAAATGGGAGTGTGCGATCACGCTTAAAAGATAATATC
30 CGTGGAGAGCCAGCATTAGACTGGTTCGAGAAGGAAGAAGATAGCGGTTGGGACAGCGAGA
GGACTAGTTTACCTACACGAGCAATGTGACCCGAAGATTATACACCGCGATGTGAAAGCA
GCTAACATTCTGTTAGATGAGGACTTCGAAGCAGTTGTTGGTGATTTTGGGTTAGCTAAG
CTTCTAGACCATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAAGTGTGGCCACATT
GCACCTGAGTACTTATCCACGGGTCAGTCCTCAGAGAAGACTGATGTCTTTGGCTTTGGC
35 ATACTTCTCCTTGAGCTCATTACTGGTCAGAAAGCTCTTGATTTTGGCAGATCCGCACAC
CAGAAAGGTGTAATGCTTGACTGGGTGAAGAAGCTGCACCAAGAAGGGAACTAAAGCAG
TTAATAGACAAAGATCTAAATGACAAGTTCGATAGAGTAGAACTCGAAGAAATCGTTCAA
GTTGCGCTACTCTGCACTCAATTCAATCCATCTCATCGACCGAAAATGTCAGAAGTTATG
AAGATGCTTGAAGGTGACGGTTTGGCTGAGAGATGGGAAGCGACGCAGAACGGTACTGGT
40 GAGCATCAGCCACCGCCATTGCCACCGGGGATGGTGAGTTCTTCGCCGCGTGTGAGGTAT

TACTCGGATTATATTTCAGGAATCGTCTCTTGTAGTAGAAGCCATTGAGCTCTCGGGTCCT
CGATGAttatgactcactgttttttaaaaaa

5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MEGVRFFVVWRLGFL
VFVWFFDISSATLSPTGVNYEV

TALVAVKNELNDP

35

YKVLENWDVNSVD

PCSWRMVSCDGYVSSL

DLPSQSLSGT

LSPRIGNLTYLQSVLQNNAITGPI

PETIGRLEKLQSLDLSNNSFTGEI

PASLGELKNLNYLRLNNSLIGTC

5 PESLSKIEGLTLVDISYNNLSGSL

PKVSARTFK VIGNALICGPK

AVSNCSAVPEPLTL

PQDGPDESGTRTNG

10

HHVALAFAASFS

AAFFVFFFTSGMFLWW

RYRRNKQIFFDVNEQYDPE

15 VSLGHLKRYTFKELRSAT

NHFNSKNILGRGGYGIVYKGHLND

GTLVAVKRLKDCNIAGGEVQFQ

TEVETISLALHRNLLRLRGFCS

20 SNQERILVYPYPNGSVASRLK

DNIRGEPALDWSRRKKIavgTA

RGLVYLHEQCdpKIIHRDVkaa

NILLDEDFEAVVGDFGLAKLLD

HRDSHVTTAVRGTVGHIAPEYL

25 STGQSSEKTDVFGFGILLLELI

TGQKALDFGRSAHQGVMLDW

VKKLHQEGKLKQLIDKDLNDKF

DRVELEEIVQVALLCTQFNPSH

RPKMSEVMKMLE

30

GDGLAERWEATQNGTGEHQPPPLPPGMVSSS

PRVRYYSdYIQESSLVVEAIELSGPR

35

Arabidopsis thaliana RKS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

Italics indicate the presence of an alternatively spliced gene product.

10

tcaattttggtagctcttagaaaa**ATGGCTCTGCTTATTATCACTGCCTTAGT**TTTTAGT
AGTTTATGGTCATCTGTGTACCAGATGCTCAAGGGGATGCATTATTTGCGTTGAGGAGC
TCGTTACGTGCATCTCCTGAACAGCTTAGTGATTGGAACCAAGTCAAGTCGATCCTTGT
ACTTGGTCTCAAGTTATTTGTGATGACAAGAAACATGTTACTTCTGTAACCTTGTCTTAC

15

ATGAACTTCTCCTCGGGAACACTGTCTTCAGGAATAGGAATCTTGACAACCTCTCAAGACT
CTTACATTGAAGGGAAATGGAATAATGGGTGGAATACCAGAATCCATTGGAAATCTGTCT
AGCTTGACCAGCTTAGATTTGGAGGATAATCACTTAACTGATCGCATTCCATCCACTCTC
GGTAATCTCAAGAATCTACAGTTCTTCAGGACCTTGAGTAGGAATAACCTTAATGGTTCT
ATCCCGGATTCACTTACAGGTCTATCAAACTGATAAATATTCTGCTCGACTCAAATAAT

20

CTCAGTGGTGAGATTCTCTCAGAGTTTATTCAAAATCCCAAATACAATTTACAGCAAAC
AACTTGAGCTGTGGTGGCACTTTCCCGCAACCTTGTGTAACCGAGTCCAGTCCTTCAGGT
GATTCAAGCAGTAGAAAACTGGAATCATCGCTGGAGTTGTTAGCGGAATAGCGGTTATT
CTACTAGGATTCTTCTTCTTTTTCTTCTGCAAGGATAAACATAAAGGATATAAACGAGAC
GTATTTGTGGATGTTGCAGGAACGAACTTTAAAAAAGGTTTGATTTTCAGGTGAAGTGGAC

25

AGAAGGATTGCTTTTGGACAGTTGAGAAGATTTCATGGAGAGAGCTTCAGTTGGCTACA
GATGAGTTCACTGAAAAGAATGTTCTCGGACAAGGAGGCTTTGGGAAAGTTTACAAAGGA
TTGCTTTTCGGATGGCACCAAAAGTCGCTGTAAAAAGATTGACTGATTTTGAACGTCCAGGA
GGAGATGAAGCTTTCCAGAGAGAAGTTGAGATGATAAGTGTAGCTGTTTCATAGGAATCTG
CTTCGCCTTATCGGCTTTTGTACAACACAACTGAACGACTTTTGGTGTATCCTTTCATG

30

CAGAATCTAAGTGTTCATATTGCTTAAGAGAGATTAAACCCGGGGATCCAGTTCTGGAT
TGGTTCAGGAGGAAACAGATTGCGTTAGGTGCAGCACGAGGACTCGAATATCTTCATGAA
CATTGCAACCCGAAGATCATAACAGAGATGTGAAAGCTGCAAATGTGTTACTAGATGAA
GACTTTGAAGCAGTGGTTGGTGATTTTGGTTTAGCCAAGTTGGTAGATGTTAGAAGGACT
AATGTAACCACTCAGGTCCGAGGAACAATGGGTCATATTGCACCAGAATGTATATCCACA

35

GGGAAATCGTCAGAGAAAACCGATGTTTTCGGGTACGGAATTATGCTTCTGGAGCTTGTA
ACTGGACAAAGAGCAATTGATTTCTCGCGGTTAGAGGAAGAAGATGATGTCTTATTGCTA
GACCATGTGAAGAACTGGAAAGAGAGAAGAGATTAGAAGACATAGTAGATAAGAAGCTT
GATGAGGATTATATAAAGGAAGAAGTTGAAATGATGATACAAGTAGCTCTGCTATGCACA
CAAGCAGCACCGGAAGAACGACCAGCGATGTCGGAAGTAGTAAGAATGCTAGAAGGAGAA

40

GGGCTTGCAGAGAGATGGGAAGAGTGGCAGAATCTTGAAGTGACGAGACAAGAAGAGTTT

CAGAGGTTGCAGAGGAGATTTGATTGGGGTGAAGATTCCATTATAATCAAGATGCTATT
GAATTATCTGGTGGAAGATAGaaacaaaaaa

5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS2 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 3 complete and 2 incomplete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site
20 for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions. Italics indicate an alternatively spliced gene
30 product.

MALLIITALVFSSL
WSSVSPDAQG

35 DALFALRSSLR
ASPEQLSDWNQNQVD

PCTWSQVICDDKKHVTSTV

T L S Y M N F S S G T L S S G I
G I L T T L K T L T L K N G I M G G I
P E S I G N L S S L T S L D L E D N H L T D R I
5 P S T L G N L K N L Q F L T L S R N N L N G S I
 P D S L T G L S K L I N I L L D S N N L S G E I
 P Q S L F K I P K Y N F T A N N L S C G G

T F P Q P C V T E S S P S G D S S S R K T G
10 I I A G V V S G I A V I L
 L G F F F F F F C

K D K H K G Y K R D V F V D V A G T N F K K G L I S G E
15 V D R R I A F G Q L R R F A W R E L Q L A T

D E F S E K N V L G Q G G F G K V Y K G L L S D
G T K V A V K R L T D F E R P G G D E A F Q
R E V E M I S V A V H R N L L R L I G F C T
20 T Q T E R L L V Y P F M Q N L S V A Y C L R
 E I K P G D P V L D W F R R K Q I A L G A A
 R G L E Y L H E H C N P K I I H R D V K A A
 N V L L D E D F E A V V G D F G L A K L V D
 V R R T N V T T Q V R G T M G H I A P E C I
25 S T G K S S E K T D V F G Y G I M L L E L V
 T G Q R A I D F S R L E E E D D V L L L D H
 V K K L E R E K R L E D I V D K K L D E D Y
 I K E E V E M M I Q V A L L C T Q A A P E E
 R P A M S E V V R M L E
30 G E G L A E R W E E W Q N L E V T R Q E E F Q

R L Q R R F D W G E D S I N N Q D A I E L S G G R

35

Arabidopsis thaliana RKS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

aacggtgaaagtttccatgatcctcttcgaggattcattcaaagaaattgctttagatgg
10 aacaatcagaaattgatcttacaatgtttc**ATGGCCTTAGCTTTTGTGGGAATCAC**TTTCG
TCAACAACTCAACCAGATATCGAAGGAGGAGCTCTGTTGCAGCTCAGAGATTCGCTTAAT
GATTCGAGCAATCGTCTAAAATGGACACGCGATTTTGTGAGCCCTTGCTATAGTTGGTCT
TATGTTACCTGCAGAGGCCAGAGTGTTGTGGCTCTAAATCTTGCCTCGAGTGGATTACACA
GGAACACTCTCTCCAGCTATTACAAAATGAAGTTCTTGGTTACCTTAGAGTTACAGAAC
15 AATAGTTTATCTGGTGCCTTACCAGATTCTCTTGGGAACATGGTTAATCTACAGACTTTA
AACCTATCAGTGAATAGTTTCAGCGGATCGATACCAGCGAGCTGGAGTCAGCTCTCGAAT
CTAAAGCACTTGGATCTCTCATCCAATAATTTAACAGGAAGCATCCCAACACAATTCTTC
TCAATCCCAACATTCGATTTTTTCAGGAACTCAGCTTATATGCGGTAAAAGTTGAATCAG
CCTTGTTCTTCAAGTTCTCGTCTTCCAGTCACATCCTCCAAGAAAAGCTGAGAGACATT
20 ACTTTGACTGCAAGTTGTGTTGCTTCTATAATCTTATTCCTTGGAGCAATGGTTATGTAT
CATCACCATCGCGTCCGCAGAACCAATACGACATCTTTTTTGTAGTAGCTGGGGAAGAT
GACAGGAAGATTTCTTTGGACAACATAAACGATTCTCTTTACGTGAAATCCAGCTCGCA
ACAGATAGTTTCAACGAGAGCAATTTGATAGGACAAGGAGGATTTGGTAAAGTATACAGA
GGTTTGCTTCCAGACAAAACAAAAGTTGCAGTGAAACGCCTTGCGGATTACTTCAGTCCT
25 GGAGGAGAAGCTGCTTTCCAAAGAGAGATTCAGCTCATAAGCGTTGCGGTTTATAAAAAT
CTCTTACGCCTTATTGGCTTCTGCACAACCTTCTCTGAGAGAATCCTTGTTTATCCATAC
ATGGAAAATCTTAGTGTTGCATATCGACTAAGAGATTTGAAAGCGGGAGAGGAAGGATTA
GACTGGCCAACAAGGAAGCGTGTAGCTTTTGGTTCAGCTCACGGTTTAGAGTATCTACAC
GAACATTGTAACCCGAAGATCATACACCGCGATCTCAAGGCTGCAAACATACTTTTAGAC
30 AACAAATTTGAGCCAGTTCTTGGAGATTTTCGGTTTAGCTAAGCTTGTGGACACATCTCTG
ACTCATGTCACAACCTCAAGTCCGAGGCACAATGGGTCACATTGCGCCAGAGTATCTCTGC
ACAGGAAAAATCATCTGAAAAAACCGATGTTTTTGGTTACGGTATAACGCTTCTTGAGCTT
GTTACTGGTCAGCGCGCAATCGATTTTTTCACGCTTGAAGAAGAGGAAAATATTCTCTTG
CTTGATCATATAAAGAAGTTGCTTAGAGAACAGAGACTTAGAGACATTGTTGATAGCAAT
35 TTGACTACATATGACTCCAAAGAAGTTGAAACAATCGTTCAAGTGGCTCTTCTCTGCACA
CAAGGCTCACCAGAAGATAGACCAGCGATGTCTGAAGTGGTCAAAATGCTTCAAGGGACT
GGTGGTTTGGCTGAGAAATGGACTGAATGGGAACAACCTGAAGAAGTTAGGAACAAAGAA
GCATTGTTGCTTCCGACTTTACCGGCTACTTGGGATGAAGAAGAAACCACGTTGATCAA
GAATCTATCCGATTATCGACAGCAAGATGAagaagaaacagagagagaaagatatctatg
40 aaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS3 protein.

- 5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a
10 leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 4 complete repeats of each
15 approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular
20 domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth
25 domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MALAFVGITSSTTQPDIEG

30

GALLQLRDSLNDSSNRL

KWTRDFVS

PCYSWSYVTCRGQSVVAL

35

NLASSGFTGTLS

P AITKLKFLVTLELQNNLSLGA

PDSLGNMVLQTLNLSVNSFSGSI

PASWSQLSNLKHLDLSSNNLTGSI
PTQFFSIPTFEFSGTQLICGKS

5 LNQPCSSSRLEPVTSSKKKLRD

ITLTASCVASIIL
FLGAMVMYHHH

10

RVRRTKYDIFFDVAGEDDR
KISFGQLKRFSLEIQLAT

DSFNESNLIGQGGFGKVYRGLLPD

15

KTKVAVKRLADYFSPGGEAAEQ
REIQLISVAVHKNLLRLIGFCT
TSSERILVYPYMENLSVAYRLR
DLKAGEEGLDWPTRKRVAFGSA
HGLEYLHEHCNPKIIHRDLKAA

20

NILLDNNFEPVLGDFGLAKLVD
TSLTHVTTQVRGTMGHIAPEYL
CTGKSSEKTDVFGYGITLLELV
TGQRAIDFSRLEEEENILLLD
HIKKLLREQRLRDIVDSNLTTY

25

DSKEVETIVQVALLCTQGSPED
RPAMSEVVKMLQ

GTGGLAEKWTEWEQLEEVNKEALLL

30

PTLPATWDEEETTVDQESIRLSTAR

Arabidopsis thaliana RKS4 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 tcttccttctccttcttggttaataatctaaagctttt**ATGGTGGT**GATGAAGATATTC
TCTGTTCTGTACTACTATGTTTCTTCGTTACTTGTCTCTCTTCTGAACCCAGAAAC
CCTGAAGTGGAGGCGTTGATAAACATAAAGAACGAGTTACATGATCCACATGGTGTTC
AAAACTGGGATGAGTTTTCTGTTGATCCTTGTAGCTGGACTATGATCTCTTGTTCCTCA
GACAACCTCGTAATTGGCTTAGGAGCTCCAAGTCAGTCTCTTTCAGGAACCTTATCTGGG
15 TCTATTGGAAATCTCACTAATCTTCGACAAGTGTCATTACAGAACAATAACATCTCCGGT
AAAATCCACCCGAGATTTGTTCTCTTCCCAAATTACAGACTCTGGATTTATCCAATAAC
CGGTTCTCCGGTGAAATCCCCGGTTCTGTTAACCAGCTGAGTAATCTCCAATATCTGTTG
AACAACAACCTCATTATCTGGGCCCTTTCCTGCTTCTCTGTCTCAAATCCCTCACCTCTCT
TTCTTAGACTTGTCTTATAACAATCTCAGAGGTCCTGTTCCCTAAATTTCTGCAAGGACA
20 TTCAATGTTGCTGGGAACCCCTTGATTTGTAAAAACAGCCTACCGGAGATTTGTTTCAGGA
TCAATCAGTGCAAGCCCTCTTCTGTCTCTTTACGTTCTTCATCAGGACGTAGAACCAAC
ATATTAGCAGTTGCACTTGGTGTAAAGCCTTGGCTTTGCTGTTAGTGTAATCCTCTCTCTC
GGGTTCAATTTGGTATCGAAAGAAACAAGACGGTTAACGATGCTTCGCATTAACAAGCAA
GAGGAAGGGTTACTTGGGTGGGAAATCTAAGAAGCTTCACATTCAGGGAACCTCATGTA
25 GCTACGGATGGTTTTAGTTCCAAGAGTATTCTTGGTGCTGGTGGGTTTGGTAATGTCTAC
AGAGGAAAATTCGGGGATGGGACAGTGGTTGCAGTGAAACGATTGAAAGATGTGAATGGA
ACCTCCGGGAACCTCACAGTTTCGTACTGAGCTTGAGATGATCAGCTTAGCTGTTCATAGG
AATTTGCTTCGGTTAATCGGTTATTGTGCGAGTTCTAGCGAAAGACTTCTTGTTTACCCT
TACATGTCCAATGGCAGCGTCGCCTCTAGGCTCAAAGCTAAGCCAGCGTTGGACTGGAAC
30 ACAAGGAAGAAGATAGCGATTGGAGCTGCAAGAGGGTTGTTTTATCTACACGAGCAATGC
GATCCCAAGATTATTCACCGAGATGTCAAGGCAGCAAACATTCTCCTAGATGAGTATTTT
GAAGCAGTTGTTGGGGATTTTGGACTAGCAAAGCTACTCAACCACGAGGATTCACATGTC
ACAACCGCGGTTAGAGGAACCTGTTGGTCACATTGCACCTGAGTATCTCTCCACCGGTCAG
TCATCTGAGAAAACCGATGTCTTTGGGTTCCGTATACTTTTGCTAGAGCTCATCACAGGA
35 ATGAGAGCTCTCGAGTTTGGCAAGTCTGTTAGCCAGAAAGGAGCTATGCTAGAATGGGTG
AGGAAGCTACACAAGGAAATGAAAGTAGAGGAGCTAGTAGACCGAGAACTGGGGACAACC
TACGATAGAATAGAAGTTGGAGAGATGCTACAAGTGGCACTGCTCTGCACTCAGTTTCTT
CCAGCTCACAGACCCAAAATGTCTGAAGTAGTTTCAAGATGCTTGAAGGAGATGGATTAGCT
GAGAGATGGGCTGCTTCACATGACCATTACATTTCTACCATGCCAACATGTCTTACAGG
40 ACTATTACCTCTACTGATGGCAACAACCAACCAACATCTGTTTGGCTCCTCAGGATTT

GAAGATGAAGATGATAATCAAGCGTTAGATTCATTCGCCATGGAACTATCTGGTCCAAGG
TAGtaaatcttggacacagaaagaaacagatataatatcccatgacttcaatttttgtt

5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS4 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MVVMKLITMKIFSVLLLL
CFFVTCSLSSEPRNPEV

EALINIKNELHDP

35

HGVFKNWDEFSVD

PCSWTMISCSSDNLVIGL

GAPSQSLSGTLS

G SIGNLTNLRQVSLQNNNISGKI
PPEICSLPKLQTLDLNNRFSGEI
PGSVNQLSNLQYLRLNNNSLSGPF
5 PASLSQIPHLSFLDLSYNNLRGPV
PKFPARTFNVAGNPLICKNS

LPEICSGSISASPL
SVSLRSSSGRRTN

10

ILAVALGVSLGFAVSVIL
SLGFIWY

RKKQRRLTMLRINKQEE
15 GLLGLGNLRSFTFRELHVAT

DGFSSKSILGAGGFGNVYRGKFGD
GTVVAVKRLKDVNGTSGNSQFR
TELEMISLAVHRNLLRLIGYCA
20 SSSERLLVYPYMSNGSVASRLK
AKPALDWNTRKKIAIGAA
RGLFYLHEQCDPKIIHRDVKAA
NILLDEYFEAVVGDFGLAKLLN
HEDSHVTTAVRGTVGHIAPEYL
25 STGQSSEKTDVFGFGILLLELI
TGMRALEFGKSVSQKGAMLEW
VRKLHKEMKVEELVDRELGTTY
DRIEVGEMLQVALLCTQFLPAH
RPKMSEVVQMLE

30

GDGLAERWAASHDHSFYHANM
SYRTITSTDGNNQTKHLFG

SSGFEDEDDNQALDSFAMELSGPR
35

Arabidopsis thaliana RKS5 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctagagaattccttatactttttctacg**ATGG**GAGATTTCCTTGATGAAGTTTCTGTTTTTA
GGAATCTGGGTTTATTATTACTCTGTTCTTGACTCTGTTTCTGCCATGGATAGTCTTTTA
TCTCCCAAGGTGGCTGCGTTAATGTCAGTGAAGAACAAGATGAAAGATGAGAAAGAGGTT
TTGTCTGGTTGGGATATTAACCTCTGTTGATCCTTGTAAGTGGAAACATGGTTGGTTGTTCT
TCTGAAGGTTTTGTGGTTTTCTCTAGAGATGGCTAGTAAAGGATTATCAGGGATACTATCT
15 ACTAGTATTGGGGAATTAACCTCATCTTCATACTTTGTTACTTCAGAATAATCAGTTAACT
GGTCCGATTCCCTCTGAGTTAGGCCAACTCTCTGAGCTTGAAACGCTTGATTTATCGGGG
AATCGGTTTAGTGTTGAAATCCCAGCTTCTTTAGGGTTCTTAACCTCACTTAACTACTTG
CGGCTTAGCAGGAATCTTTTATCTGGGCAAGTCCCTCACCTCGTCGCTGGCCTCTCAGGT
CTTTCTTTCTTGGATCTATCTTTCAACAATCTAAGCGGACCAACTCCGAATATATCAGCA
20 AAAGATTACAGGAAATGCATTTCTTTGTGGTCCAGCTTCCCAAGAGCTTTGCTCAGATGC
TACACCTGTGAGAAATGCTGCAATCGATCTGCAGCGACGGGTTTGTCTGAAAAGGACAAT
AGCAAACATCACAGCTTAGTGCTCTCTTTTGCATTTGGCATTGTTGTTGCCTTTATCATC
TCCCTAATGTTTCTCTTCTCTGGGTGCTTTGGCATCGATCACGTCTCTCAAGATCACAC
GTGCAGCAAGACTACGAATTTGAAATCGGCCATCTGAAAAGGTTCAAGTTTTCGCGAAATA
25 CAAACCGCAACAAGCAATTTTAGTCCAAAGAACATTTTGGGACAAGGAGGGTTTGGGATG
GTTTATAAAGGGTATCTCCCAAATGGAAGTGTGGTGGCAGTTAAAAGATTGAAAGATCCG
ATTTATACAGGAGAAGTTCAAGTTTCAAACCGAAGTAGAGATGATTGGCTTAGCTGTTTAC
CGTAACCTTTTACGCCTCTTTGGATTCTGTATGACCCCGAAGAGAGAATGCTTGTGTAT
CCGTACATGCCAAATGGAAGCGTAGCTGATCGTCTGAGAGATTGGAATCGGAGGATAAGC
30 ATTGCACTCGGCGCAGCTCGAGGACTTGTTTACTTGACGAGCAATGCAATCCAAAGATT
ATTCACAGAGACGTCAAAGCTGCAAATATTCTACTTGATGAGAGCTTTGAAGCAATAGTT
GGCGATTTTGGTCTAGCAAAGCTTTTAGACCAGAGAGATTACATGTCACTACCGCAGTC
CGAGGAACCATTTGGACACATCGCTCCCGAGTACCTTTCCACTGGACAGTCCTCAGAGAAA
ACCGATGTTTTCGGATTCGGAGTACTAATCCTTGAAGTATAACAGGTCATAAGATGATT
35 GATCAAGGCAATGGTCAAGTTCGAAAAGGAATGATATTGAGCTGGGTAAGGACATTGAAA
GCAGAGAAGAGATTTCAGAGATGGTGGACAGAGATTGAAAGGAGAGTTTGATGATTG
GTGTTGGAGGAAGTAGTGAATTGGCTTTGCTTTGTACACAGCCACATCCGAATCTAAGA
CCGAGGATGTCTCAAGTGTGGAAGGTACTAGAAGGTTTAGTGGAACAGTGTGAAGGAGGG
TATGAAGCTAGAGCTCCAAGTGTCTCTAGGAAGTACAGTAATGGTCATGAAGAGCAGTCC
40 TTTATTATTGAAGCCATTGAGCTCTCTGGACCACGATGatagacttcatagtgtcttaac

tagtcttcttgattttgttgatcattgtcatggc

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS5 protein.

5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains no
10 leucine zipper motif, in contrast to the other RKS proteins. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues.
15 The fifth domain contains many serine residues, and is likely to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine /
20 threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein /
25 protein interactions.

MEISLMKFLFLGIWVYYYS

VLDSVSAMDSLLSPKV

30

AALMSVKNMKDE

KEVLSGWDINSVD

PCTWNMVGCSSEGFVVS

35

LEMASKGLSGILS

T SIGELTHLHTLLLQNNQLTGPI

PSELGQLSELETLDLSGNRFSGEI

PASLGFLTHLNYLRNLLSGQV

PHLVAGLSGLSFLDLSFNNLSGPT
PNISAK DYRK CISLWSSFPR

ALLRCYTCEKCCNR

5 SAATGLSEKDNSK

HHSLVLSFAFGIVV
AFIISLMFLFFWVLWH

10 RSRLSRSHVQQDYEF
EIGHLKRFSFREIQTAT

SNFSPKNILGQGGFGMVYKGYLPN
GTVVAVKRLKDPIYTGEVQFQ

15 TEVEMIGLAVHRNLLRFLGFCM
TPEERMLVYPMPNGSVADRLR
DWNRRISIALGAA

RGLVYLHEQCNPKIIHRDVKAA
NILLDESFEAIVGDFGLAKLLD
20 QRD SHVTTAVRG TIGHIAPEYL
STGQSSEKTDVFGFVLI LELI
TGHKMIDQNGQVRKGMILSW
VRTLKA EKRF AEMVDRDLKGEF
DDLVL EEVVELALLCTQPHPNL

25 RPRMSQVLKV

LEGLVEQCEGGYEARA

PASVSRNYSNGHEEQSFII EAIELSGPR

30

Arabidopsis thaliana RKS6 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

```
attgttttccttcttttgggattttctccttggatggaaccagctcaattaatgagatgag
10 ATGAGAATGTTCAGCTTGCAGAAGATGGCTATGGCTTTTACTCTCTTGTTTTTGCCTGT
TTATGCTCATTGTGTCTCCAGATGCTCAAGGGGATGCACTGTTTGCGTTGAGGATCTCC
TTACGTGCATTACCGAATCAGCTAAGTGACTGGAATCAGAACCAAGTTAATCCTTGCACT
TGGTCCCAAGTTATTTGTGATGACAAAACTTTGTCACCTCTCTTACATTGTCAGATATG
AACTTCTCGGGAACCTTGTCTTCAAGAGTAGGAATCCTAGAAAATCTCAAGACTCTTACT
15 TTAAAGGGAAATGGAATTACGGGTGAAATACCAGAAGACTTTGGAAATCTGACTAGCTTG
ACTAGTTTGGATTGGAGGACAATCAGCTAACTGGTGTATACCATCCACTATCGGTAAT
CTCAAGAACTTCAGTTCTTGACCTTGAGTAGGAACAACTTAATGGGACTATTCCGGAG
TCACTCACTGGTCTTCCAAACCTGTTAAACCTGCTGCTTGATTCCAATAGTCTCAGTGGT
CAGATTCCCTCAAAGTCTGTTTGAGATCCCCAAATATAATTTACGTCAAACAACTTGAAT
20 TGTGGCGGTCGTCAACCTCACCCCTTGTGTATCCGCGGTTGCCCATTCAGGTGATTCAAGC
AAGCCTAAAACTGGCATTATTGCTGGAGTTGTTGCTGGAGTTACAGTTGTTCTCTTTGGA
ATCTTGTTGTTTCTGTTCTGCAAGGATAGGCATAAAGGATATAGACGTGATGTGTTTG
GATGTTGCAGGTGAAGTGGACAGGAGAATTGCATTTGGACAGTTGAAAAGGTTTGCATGG
AGAGAGCTCCAGTTAGCGACAGATAACTTCAGCGAAAAGAATGTACTTGGTCAAGGAGGC
25 TTTGGGAAAGTTTACAAAGGAGTGCTTCCGGATACACCCAAAGTTGCTGTGAAGAGATTG
ACGGATTTCGAAAGTCTTGGTGGAGATGCTGCTTTCCAAAGGGAAGTAGAGATGATAAGT
GTAGCTGTTTCATAGGAATCTACTCCGTCTTATCGGGTTCTGCACCACACAAACAGAACGC
CTTTTGGTTTATCCCTTCATGCAGAATCTAAGTCTTGACATCGTCTGAGAGAGATCAAA
GCAGGCGACCCGGTTCTAGATTGGGAGACGAGGAAACGGATTGCCTTAGGAGCAGCGCGT
30 GGTTTTGAGTATCTTCATGAACATTGCAATCCGAAGATCATACATCGTGATGTGAAAGCA
GCTAATGTGTTACTAGATGAAGATTTTGAAGCAGTGGTTGGTGATTTTGGTTTAGCCAAG
CTAGTAGATGTTAGAAGGACTAATGTGACTACTCAAGTTCGAGGAACAATGGGTACATT
GCACCAGAATATTTATCAACAGGGAAATCATCAGAGAGAACCGATGTTTTCGGGTATGGA
ATTATGCTTCTTGAGCTTGTTACAGGACAACGCGCAATAGACTTTTCACGTTTGGAGGAA
35 GAAGATGATGTCTTGTTACTTGACCACGTGAAGAACTGGAAAGAGAGAAGAGATTAGGA
GCAATCGTAGATAAGAATTTGGATGGAGAGTATATAAAAGAAGAAGTAGAGATGATGATA
CAAGTGGCTTTGCTTTGTACACAAGGTTACCAGAAGACCGACCGAGTGATGTCTGAAGTT
GTGAGGATGTTAGAAGGAGAAGGGCTTGCGGAGAGATGGGAAGAGTGGCAAACGTGGAA
GTCACGAGACGTCATGAGTTTGAACGGTTGCAGAGGAGATTTGATTGGGGTGAAGATTCT
40 ATGCATAACCAAGATGCCATTGAATTATCTGGTGGAAGATGAccaaaaacatcaaacctt
```

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS6 protein.

Different domains are spaced and shown from the N-terminus
5 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each
10 separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain
15 contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown
20 function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single
25 leucine rich repeat, probably involved in protein / protein interactions.

MRMFSL

QKMAMAF¹TL²LLFFAC³LC⁴SVSPDAQ⁵G

30

DALFALRISLRALP

NQLSDWNQNQVN

PCTWSQVICDDKNFV¹TSL

35

TLSDMN¹FSGTLSSRV

GILENLK¹TL²TLKNGITGEI

PEDFGN¹LTSL²SLDLEDNQLTGRI

PSTIGNLKKLQFLTLNRKLNGTI
PESLTGLPNLLNLLLDNSLSGQI
PQSLFEIPKYNFTSNNLNCGG

5 RQPHPCVSAVAHSGDSSKPKTG

IIAGVVAGVTVVL
FGILLEFLFC

10 KDRHKGYYRDDVFVDVAGE
VDRRIAFIGQLKRFARRELQLAT

DNFSEKNVLGQGGFGKVYKGVLPD
TPKVAVKRLTDFESPGDAAFO

15 REVEMISVAVHRNLLRLIGFCT
TQTERLLVYPFMQNLSLAHLR
EIKAGDPVLDWETRKRIALGAA
RGFEYLHEHCNPKIIHRDVKAA
NVLLDEDFEAVVGDFGLAKLVD

20 VRRTNVTTQVRGTMGHIAPEYL
STGKSSERTDVFGYGIMLLELV
TGQRAIDFSRLEEDDVLLLDH
VKKLEREKRLGAIVDKNLDGEY
IKEEVEMMIQVALLCTQGSPED

25 RPVMSEVVRMLE

GEGLAERWEEWQNEVTRRHEFE

RLQRRFDWGEDSMHNQDAIELSGGR

30

Arabidopsis thaliana RKS7 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 acatcttggtttctgctcattcctctgtttcaaca**ATGGAGAGT**ACTATTGTTATGATGA
TGATGATAACAAGATCTTTCTTTGCTTCTTGGGATTTTATGCCTTCTCTGCTCTTCTG
TTCACGGATTGCTTTCTCCTAAAGGTGTTAACTTTGAAGTGCAAGCTTTGATGGACATAA
AAGCTTCATTACATGATCCTCATGGTGTTCTTGATAACTGGGATAGAGATGCTGTTGATC
CTTGTAGTTGGACAATGGTCACTTGTTCTTCTGAAAACCTTTGTCATTGGCTTAGGCACAC
15 CAAGTCAGAATTTATCTGGTACACTATCTCCAAGCATTACCACTTAACAAATCTTCGGA
TTGTGCTGTTGCAGAACAAACATAAAAGGAAAAATTCCTGCTGAGATTGGTCGGCTTA
CGAGGCTTGAGACTCTTGATCTTTCTGATAATTTCTTCCACGGTGAAATTCCTTTTTTCAG
TAGGCTATCTACAAAGCCTGCAATATCTGAGGCTTAACAACAATTCTCTCTCTGGAGTGT
TTCCTCTGTCACTATCTAATATGACTCAACTTGCCTTTCTTGATTTATCATACAACAATC
20 TTAGTGGTCCTGTTCCAAGATTGCTGCAAAGACGTTTAGCATCGTTGGGAACCCGCTGA
TATGTCCAACGGGTACCGAACCAGACTGCAATGGAACAACATTGATACCTATGTCTATGA
ACTTGAATCAAACCTGGAGTTCCCTTTATACGCCGGTGGATCGAGGAATCACAAAATGGCAA
TCGCTGTTGGATCCAGCGTTGGGACTGTATCATTAATCTTCATTGCTGTTGGTTGTTTC
TCTGGTGGAGACAAAGACATAACCAAAACACATTCTTTGATGTTAAAGATGGGAATCATC
25 ATGAGGAAGTTTCACTTGGAAACCTGAGGAGATTGGTTTCAGGGAGCTTCAGATTGCCA
CCAATAAAGTTTCACTTGGAAACCTGAGGAGATTGGTTTCAGGGAGCTTCAGATTGCCA
GAATACTTGGAGATAGTACAGTGGTTGCAGTGAAAAGGCTTAAAGATGGAGGAGCATTGG
GAGGAGAGATTGAGTTTCAGACAGAAGTTGAAATGATCAGTTTAGCTGTTTCATCGAAATC
TCTTAAGACTCTACGGTTTCTGCATCACACAACTGAGAAGCTTCTAGTTTATCCTTATA
30 TGTCTAATGGAAGCGTTGCATCTCGAATGAAAGCAAAACCTGTTCTTGACTGGAGCATAA
GGAAGAGGATAGCCATAGGAGCTGCAAGAGGGCTTGTGTATCTCCATGAGCAATGTGATC
CGAAGATTATCCACCGCGATGTCAAAGCAGCGAATATACTTCTTGATGACTACTGTGAAG
CTGTGGTTGGCGATTTTGGTTTAGCTAAACTCTTGGATCATCAAGATTCTCATGTGACAA
CCGCGGTTAGAGGCACGGTGGGTACATTGCTCCAGAGTATCTCTCAACTGGTCAATCCT
35 CTGAGAAAACAGATGTTTTTGGCTTCGGGATTCTTCTTCTTGAGCTTGTAACCGGACAAA
GAGCTTTTGGAGTTTGGTAAAGCGGCTAACAGAAAGGTGTGATGCTTGATTGGGTAAAAA
AGATTCATCAAGAGAAGAACTTGAGCTACTTGTGGATAAAGAGTTGTTGAAGAAGAAGA
GCTACGATGAGATTGAGTTAGACGAAATGGTAAGAGTAGCTTTGTTGTGCACACAGTACC
TGCCAGGACATAGACCAAAAATGTCTGAAGTTGTTTGAATGCTGGAAGGAGATGGACTTG
40 CAGAGAAATGGGAAGCTTCTCAAAGATCAGACAGTGTTTCAAATGTAGCAACAGGATAA

ATGAATTGATGTCATCTTCAGACAGATACTCTGATCTTACCGATGACTCTAGTTTACTTG
TGCAAGCAATGGAGCTCTCTGGTCCTAGATGAaatctatacatgaatctgaagaagaaga
agaacatgcatctgtttcttgaatcaagagggattcttgtttttttgtataatagagagg
ttttttggaggggaaatgttgtgtctctgtaactgtataggcttgttgtgtaagaagttat
5 tactgcacttaggggttaattcaaagttctttacataaaaaaatgattagttgcgttgaata
gaggggaacactttgggagatttcatgtatgaaatttggaaaaaaaaaaaaaaaaaaaaaa

10 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS7 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

15 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
20 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
25 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
30 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

35

MESTIVMMMITRSFF

CFLGFLCLLCSSVHGLLSPKGVNFEV

QALMDIKASLHDP
HGVLDNWDRAVD

PCSWTMVTCSSNFVIG

5

LGTPSQNLSGTL
SPSITNLTLNRIVLLQNNNIKGKI
PAEIGRLTRLETLDLSDNFFHGEI
PFSVGYLQSLQYLRLNNSLSGVF
10 PLSLSNMTQLAFDLDSYNNLSGPV
PRFAA KTFIVGNPLICPT

GTEPDCNGTTLIPMSMNL
NQTGVPLYAGGSRNHKMA

15

IAVGSSVGTVSLIFIAVGLFLWW

RQRHNQNTFFDVKGDNHHE
EVSLGNLRRFGFRELQIAT

20

NNFSSKNLLGKGGYGNVYKGILGD
STVVAVKRLKDGGALGGEIQFO
TEVEMISLAVHRNLLRLYGFCI
TQTEKLLVYPYMSNGSVA

25

SRMKAKPVLDSIRKRIAIGAA
RGLVYLHEQCDPKIIHRDVKAA
NILLDDYCEAVVGDFGLAKLLD
HQDSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELV

30

TGQRAFEFGKAANQKGVMLDW
VKKIHQEKLELLVDKELLKKKSY
DEIELDEMVRVALLCTQYLPGH
RPKMSEVVRMLE

35

GDGLAEKWEASQRSDS
VSKCSNRINELMSSS

DRYSDLTDDSSLLVQAMELSGPR

40

Arabidopsis thaliana RKS8 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 gttttttttttttaccctcttggaggatctgggaggagaaatttgcttttttttggttaa
ATGGGGAGAAAAAGTTTGAAGCTTTTGGTTTTGTCTGCTTAATCTCACTGCTTCTTCTG
TTTAATTCGTTATGGCTTGCCTCTTCTAACATGGAAGGTGATGCACTGCACAGTTTGAGA
GCTAATCTAGTTGATCCAAATAATGTCTTGCAAAGCTGGGATCCTACGCTTGTTAATCCG
TGTACTTGGTTTCACGTAACGTGTAACAACGAGAACAGTGTTATAAGAGTCGATCTTGGG
15 AATGCAGACTTGTCTGGTCAGTTGGTTCCTCAGCTAGGTCAGCTCAAGAACTTGCAGTAC
TTGGAGCTTTATAGTAATAACATAACCGGGCCGGTTCCAAGCGATCTTGGGAATCTGACA
AACTTAGTGAGCTTGGATCTTTACTTGAACAGCTTCACTGGTCCAATTCCAGATTCTCTA
GGAAAGCTATTCAAGCTTCGCTTTCTTCGGCTCAACAATAACAGTCTCACCGGACCAATT
CCCATGTCATTGACTAATATCATGACCCTTCAAGTTTTGGATCTGTGGAACAACCGATTA
20 TCCGGATCTGTTCCCTGATAATGGTTCCTTCTCGCTCTTCACTCCCATCAGTTTGCTAAC
AACTTGGATCTATGCGGCCAGTTACTAGCCGTCCTTGTCTGGATCTCCCCGTTTTCT
CCTCCACCACCTTTTATACCACCTCCCATAGTTCTTACACCAGGTGGGTATAGTGCTACT
GGAGCCATTGCGGGAGGAGTTGCTGCTGGTGCTGCTTTACTATTTGCTGCCCCTGCTTTA
GCTTTTGCTTGGTGGCGTAGAAGAAAACCTCAAGAATTCTTCTTTGATGTTCTTGCCGAA
25 GAGGACCCTGAGGTTCACTTGGGGCAGCTTAAGCGGTTCTCTCTACGGGAACCTCAAGTA
GCAACTGATAGCTTCAGCAACAAGAACATTTTGGGCCGAGGTGGGTTTCGAAAAAGTCTAC
AAAGGCCGTCTTGCTGATGGAACACTTGTTGCAGTCAAACGGCTTAAAGAAGAGCGAACC
CCAGGTGGCGAGCTCCAGTTTCAGACAGAAGTGGAGATGATAAGCATGGCCGTTACAGA
AATCTCCTCAGGCTACGCGGTTTCTGTATGACCCCTACCGAGAGATTGCTTGTTTATCCT
30 TACATGGCTAATGGAAGTGTCGCTTCTGTTTGAGAGAACGTCCACCATCACAGTTGCCT
CTAGCCTGGTCAATAAGACAGCAAATCGCGCTAGGATCAGCGAGGGGTTTGTCTTATCTT
CATGATCATTGCGACCCCAAAATTATTCACCGTGATGTGAAAGCTGCTAATATTCTGTTG
GACGAGGAATTTGAGGCGGTGGTAGGTGATTTCGGGTTAGCTAGACTTATGGACTATAAA
GATACTCATGTCAACCGGCTGTGCGTGGGACTATTGGACACATTGCTCCTGAGTATCTC
35 TCAACTGGAAAATCTTCAGAGAAAACCTGATGTTTTTGGCTACGGGATCATGCTTTTGAA
CTGATTACAGGTCAGAGAGCTTTTGATCTTGCAAGACTGGCGAATGACGATGACGTTATG
CTCCTAGATTGGGTGAAAGGGCTTTTGAAGGAGAAGAAGCTGGAGATGCTTGTGGATCCT
GACCTGCAAAGCAATTACACAGAAGCAGAAGTAGAACAGCTCATACAAGTGGCTCTTCTC
TGCACACAGAGCTCACCTATGGAACGACCTAAGATGTCTGAGGTTGTTGGAATGCTTGAA
40 GGTGACGGTTTAGCGGAGAAATGGGACGAGTGGCAGAAAGTGGAAGTTCTCAGGCAAGAA

GTGGAGCTCTCTTCTCACCCACCTCTGACTGGATCCTTGATTGCGACTGATAATCTTCAT
GCTATGGAGTTGTCTGGTCCAAGATAAacgacattgtaatttgcctaacagaaaagagaa
agaacagagaaatattaagagaatcacttctctgtattctt

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS8 protein.

10 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30 MGRKKFEAFGFVCLISLLLLFNSL
WLASSNMEG

DALHSLRANLVDP
NNVLQSWDPTLVN

35

PCTWFHVTCNNNSVIRV

DLGNADLSGQLV

P QLGQLKNLQYLELYSNNITGPV
40 PSDLGNLTNLVSLDLYLNSFTGPI

PDSLGLKLFKLRFLRLNNNSLTGPI
PMSLTNIMTLQVLDLSNNRLSGSV
PDNGSFSLFTPISFANNLDLCGPV

5 TSRPCPGSPPFSPPPP
 FIPPPIVPTPGGYSATG

AIAGGVAAGAAL
LFAAPALAFAWW

10 RRRKPQEFFFDPVPAEEDPE
 VHLGQLKRFSLRELQVAT

DSFSNKNILGRGGFGKVYKGRLAD
15 GTLVAVKRLKEERTPGGELQFQ
 TEVEMISMAVHRNLLRLRGFCM
 TPTERLLVYPYMANGSVASCLR
 ERPPSQLPLAWSIRQQIALGSA
 RGLSYLHDHCDPKIIHRDVKAA

20 NILLDEEFEAVVGDFGLARLMD
 YKDTHVTTAVRGTTIGHIAPEYL
 STGKSSEKTDVFGYGIMLLELI
 TGQRAFDLARLANDDDVMLLDW
 VKGLLKEKKLEMLVDPDLQSNY

25 TEAEVEQLIQVALLCTQSSPME
 RPKMSEVVRMLE

GDGLAEKWDEWQKVEVLRQEVELS

30 SHPTSDWILDSTDNLHAMELSGPR

Arabidopsis thaliana rks10 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atcagggggtttaacaatgatggatctctctgatgagggatagttctagggtttgtttt
taatctcttgaggataaaa**ATGGAACGAAGATTAATGATCCCTTGCTTCTTTTGGTTGATT**
CTCGTTTTGGATTTGGTTCTCAGAGTCTCGGGCAACGCCGAAGGTGATGCTCTAAGTGCA
CTGAAAAACAGTTTAGCCGACCCTAATAAGGTGCTTCAAAGTTGGGATGCTACTCTTGTT
ACTCCATGTACATGGTTTCATGTTACTTGCAATAGCGACAATAGTGTTACACGTGTTGAC
15 CTTGGGAATGCAAATCTATCTGGACAGCTCGTAATGCAACTTGGTCAGCTTCCAACTTG
CAGTACTTGGAGCTTTATAGCAATAACATTACTGGGACAATCCCAGAACAGCTTGGAAAT
CTGACGGAATTGGTGAGCTTGGATCTTTACTTGAACAATTTAAGCGGGCCTATTCCATCA
ACTCTCGGCCGACTTAAGAACTCCGTTTCTTGCGTCTTAATAACAATAGCTTATCTGGA
GAAATTCCAAGGTCTTTGACTGCTGTCTTGACGCTACAAGTTCTGGATCTCTCAAACAAT
20 CCTCTCACCGGAGATATTCTGTAAATGGTTCCTTTTCACTTTTCACTCCAATCAGTTTT
GCCAACACCAAGTTGACTCCCCCTTCCTGCATCTCCACCGCCTCCTATCTCTCCTACACCG
CCATCACCTGCAGGGAGTAATAGAATTACTGGAGCGATTGCGGGAGGAGTTGCTGCAGGT
GCTGCACTTCTATTTGCTGTTCCGGCCATTGCACCTAGCTTGGTGGCGAAGGAAAAAGCCG
CAGGACCACTTCTTTGATGTACCAGCTGAAGAGGACCCAGAAGTTCATTTAGGACAACCTG
25 AAGAGGTTTTTCATTGCGTGAACTACAAGTTGCTTCGGATAATTTTAGCAACAAGAACATA
TTGGGTAGAGGTGGTTTTTGGTAAAGTTTATAAAGGACGGTTAGCTGATGGTACTTTTAGTG
GCCGTTAAAAGGCTAAAAGAGGAGCGCACCCAAGGTGGCGAACTGCAGTTCAGACAGAG
GTTGAGATGATTAGTATGGCGGTTACAGAACTTGCTTCGGCTTCGTGGATTTTGCATG
ACTCCAACCGAAAGATTGCTTGTTTATCCCTACATGGCTAATGGAAGTGTTGCCCTCCTGT
30 TTAAGAGAACGTCCCGAGTCCCAGCCACCACTTGATTGGCCAAAGAGACAGCGTATTGCC
TTGGGATCTGCAAGAGGGCTTGCGTATTTACATGATCATTGCGACCCAAAGATTATTCAT
CGAGATGTGAAAGCTGCAAATATTTTGTGGATGAAGAGTTTGAAGCCGTGGTTGGGGAT
TTTGGACTTGCAAACTCATGGACTACAAAGACACACATGTGACAACCGCAGTGCGTGGG
ACAATTGGTCATATAGCCCCTGAGTACCTTTCCACTGGAAAATCATCAGAGAAAACCGAT
35 GTCTTTGGGTATGGAGTCATGCTTCTTGAGCTTATCACTGGACAAAGGGCTTTTGATCTT
GCTCGCCTCGCGAATGATGATGATGTGATGTTACTAGACTGGGTGAAAGGGTTGTTAAAA
GAGAAGAAATTGGAAGCACTAGTAGATGTTGATCTTCAGGGTAATTACAAAGACGAAGAA
GTGGAGCAGCTAATCCAAGTGGCTTTACTCTGCACTCAGAGTTCACCAATGGAAAGACCC
AAAATGTCTGAAGTTGTAAGAATGCTTGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAG
40 TGGCAAAAGGAGGAAATGTTTACAGACAAGATTTCAACTACCCAACCCACCATCCAGCCGTG

TCTGGCTGGATCATTGGCGATTCCACTTCCCAGATCGAAAACGAATACCCCTCGGGTCCA
AGATAA gatttcgaaacacgaatgttttttctgtattttgtttttctctgtattttattgag
ggtttttagcttc

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS10 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as
described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a
signal sequence. The second domain contains a leucine zipper motif,
containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues,
involved in disulphate bridge formation. The fourth domain contains a
leucine rich repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain contains many
serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain
contains a single transmembrane domain after which the predicted
intracellular domains are positioned. The seventh domain has an
unknown function. The eight domain represents a serine / threonine
protein kinase domain (Schmidt et al. 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth
domain has an unknown function. The last and tenth domain at the C-
terminal end represents part of a single leucine rich repeat,
probably involved in protein / protein interactions.

30 MERRLMIPCFFWLILVL
DLVLRVSGNAEG

DALSALKNSLADP
NKVLQSWDATLVT

35

PCTWFHVTCNSDNSVTRV

DLGNANLSGQLV

M QLGQLPNLQYLELYSNNITGTI

40

PEQLGNLTSLVSLDLYLNNLSGPI

PSTLGRLKKLRFLRLNNSLSGEI
PRSLTAVLTLQVLDLSNNPLTGDI
PVNGSFSLTPISFANTK LT PL

5 PASPPPPISPTPPSPAGSNRITG

AIAGGVAAGAAL
LFAVPAIALAWW

10 RRKKPQDHFFDVPAEEDPE
VHLGQLKRFSLRELQVAS

DNFSNKNILGRGGFGKVYKGRAD

GTLVAVKRLKEERTQGGELOFQ

15 TEVEMISMAVHRNLLRLRGFCM

TPTERLLVYPYMANGSVASCLR

ERPESQPPLDWPKRQRIALGSA

RGLAYLHDHCDPKIIHRDVKAA

NILLDEEFEAVVGDFGLAKLMD

20 YKDTHVTTAVRGTIIGHIAPEYL

STGKSSEKTDVFGYGVMLELI

TGQRAFDLARLANDDDVMLLDW

VKGLLKEKKLEALVDVDLQGNV

KDEEVEQLIQVALLCTQSSPME

25 RPKMSEVVRMLE

GDGLAERWEEWQKEEMFRQDFNYPTH

PAVSGWIIIGDSTSQIENEYPSGPR

30

Arabidopsis thaliana RKS 11 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttgttaacctctcgtaactaaaatcttcc**ATGG**TAGTAGTAACAAAGAAGACCATGAAGA
TTCAAATTCATCTCCTTTACTCGTTCTTGTTCCCTCTGTTTCTCTACTCTCACTCTATCTT
CTGAGCCCAGAAACCTGAAGTTGAGGCGTTGATAAGTATAAGGAACAATTTGCATGATC
CTCATGGAGCTTTGAACAATTGGGACGAGTTTTTCAGTTGATCCTTGAGCTGGGCTATGA
TCACTTGCTCTCCCGACAACCTCGTCATTGGACTAGGAGCGCCGAGCCAGTCTCTCTCGG
15 GAGGTTTATCTGAGTCTATCGGAAATCTCACAAATCTCCGACAAGTGTCATTGCAAAATA
ACAACATCTCCGGCAAAATTCACCGGAGCTCGGTTTTCTACCCAAATTACAAACCTTGG
ATCTTTCCAACAACCGATTCTCCGGTGACATCCCTGTTTCCATCGACCAGCTAAGCAGCC
TTCAATATCTGAGACTCAACAACAACCTCTTGTCTGGGCCCTTCCCTGCTTCTTTGTCCC
AAATTCCTCACCTCTCCTTCTTGGAAGTTGTCTTACAACAATCTCAGTGGCCCTGTTCTTA
20 AATTCACAGCAAGGACTTTAAACGTTGCTGGTAATCCTTTGATTGTAGAAGCAACCCAC
CTGAGATTTGTTCTGGATCAATCAATGCAAGTCCACTTTCTGTTTCTTTGAGCTCTTCAT
CAGGACGCAGGTCTAATAGATTGGCAATAGCTCTTAGTGTAAGCCTTGGCTCTGTTGTTA
TACTAGTCCTTGCTCTCGGGTCCTTTTGTGGTACCGAAAGAAACAAAGAAGGCTACTGA
TCCTTAACTTAAACGCAGATAAACAAGAGGAAGGGCTTCAAGGACTTGGGAATCTAAGAA
25 GCTTCACATTCAGAGAACTCCATGTTTATACAGATGGTTTTAGTTCCAAGAACATTCTCG
GCGCTGGTGGATTCCGTAATGTGTACAGAGGCAAGCTTGGAGATGGGACAATGGTGGCAG
TGAAACGGTTGAAGGATATTAATGGAACCTCAGGGGATTCACAGTTTCGTATGGAGCTAG
AGATGATTAGCTTAGCTGTTTATAAGAATCTGCTTCGGTTAATTGGTTATTGCGCAACTT
CTGGTGAAAGGCTTCTTGTTTACCCTTACATGCCTAATGGAAGCGTCGCCTCTAAGCTTA
30 AATCTAAACCGGCATTGGACTGGAACATGAGGAAGAGGATAGCAATTGGTGCAGCGAGAG
GTTTGTGTATCTACATGAGCAATGTGATCCCAAGATCATTATAGAGATGTAAAGGCAG
CTAATATTCTCTTAGACGAGTGCTTTGAAGCTGTTGTTGGTGACTTTGGACTCGCAAAGC
TCCTTAACCATGCGGATTCTCATGTCACAACCTGCGGTCCGTGGTACGGTTGGCCACATTG
CACCTGAATATCTCTCCACTGGTCAGTCTTCTGAGAAAACCGATGTGTTTGGGTTCCGGTA
35 TACTATTGCTCGAGCTCATAACCGGACTGAGAGCTCTTGAGTTTGGTAAAACCGTTAGCC
AGAAAGGAGCTATGCTTGAATGGGTGAGGAAATTACATGAAGAGATGAAAGTAGAGGAAC
TATTGGATCGAGAACTCGGAACCTAAGTACGATAAGATTGAAGTTGGAGAGATGTTGCAAG
TGGCTTTGCTATGCACACAATATCTGCCAGCTCATCGTCTAAAATGTCTGAAGTTGTTT
TGATGCTTGAAGGCGATGGATTAGCCGAGAGATGGGCTGCTTCGCATAACCATTACATT
40 TCTACCATGCCAATATCTCTTTCAAGACAATCTCTTCTCTGTCTACTACTTCTGTCTCAA

GGCTTGACGCACATTGCAATGATCCAACCTTATCAAATGTTTGGATCTTCGGCTTTTCGATG
ATGACGATGATCATCAGCCTTTAGATTCCTTTGCCATGGAACCTATCCGGTCCAAGATAAc
acaatgaaagaaagatatcattttttacgatggatcaaacaatccaatgaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS11 protein.

10 Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
15 leucine zipper motif, containing 3 leucine residues, each
separated by seven other amino acids. The third domain
contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
20 approximately 24 amino acid residues. The fifth domain
contains many serine and proline residues, and is likely to
contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
25 domains are positioned. The seventh domain has an unknown
function. The eighth domain represents a serine / threonine
protein kinase domain (Schmidt *et al.* 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
30 domain at the C-terminal end represents part of a single
leucine rich repeat, probably involved in protein / protein
interactions.

MVVVTKKTMKIQIHLLYSFLFL
35 CFSTLTLSSEPRNPEV

EALISIRNNLHDP
HGALNNWDEFSVD

PCSWAMITCSPDNLVIGL

GAPSQSLSGGLS

5 ESIGNLTNLQVSLQNNNISGKI
PPELGFLPKLQTLDLNNRFSGDI
PVSIDQLSSLQYLRNNNSLSGPF
PASLSQIPHLSFLDLSYNNLSGPV
PKFPARTFNVAGNPLICRSN

10

PPEICSGSINASPL
SVSLSSSSGRRSNR

LAIALSVSLGSVVIL

15

VLALGSFCWY

RKKQRLLIILNLNGADKQEE
GLQGLGNLRSFTFRELHVYT

20

DGFSSKNILGAGGFGNVYRGKLG
GTMVAVKRLKDINGTSGDSQFR
MELEMISLAVHKNLLRLIGYCA
TSGERLLVYPMPNGSVASKLK
SKPALDWNMRKRIAIGAA

25

RGLLYLHEQCDPKIIHRDVKAA
NILLDECFEAVVGDFGLAKLLN
HADSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLELI
TGLRALEFGKTVSQKGAMLEW

30

VRKLHEEMKVEELLDRELGTNY
DKIEVGEMLQVALLCTQYLP
RPMSEVVLML

GDGLAERWAASHNHSHFYHANI

35

SFKTISSLSTTSVSRDLAHCNDPTYQMFG

SSAFDDDDDHQPLDSFAMELSGPR

Arabidopsis thaliana RKS12 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 tttaaaaaccttgctagttctcaattctcatgactttgcttttagtcttagaagtggaaa
ATGGAACATGGATCATCCCGTGGCTTTATTTGGCTGATTCTATTTCTCGATTTTGTTC
AGAGTCACCGGAAAAACACAAGTTGATGCTCTCATTGCTCTAAGAAGCAGTTTATCATCA
GGTGACCATACAAACAATATACTCCAAAGCTGGAATGCCACTCACGTTACTCCATGTTCA
TGGTTTCATGTTACTTGCAATACTGAAAACAGTGTTACTCGTCTTGACCTGGGGAGTGCT
15 AATCTATCTGGAGAACTGGTGCCACAGCTTGCTCAGCTTCCAAATTTGCAGTACTTGAA
CTTTTAAACAATAATATTACTGGGGAGATACCTGAGGAGCTTGCGGACTTGATGGAAC
GTAAGCTTGACCTTTTGGCAAACAACATAAGCGGTCCCATCCCTTCTCTCTGGCAAA
CTAGGAAAACCTCCGCTTCTTGCGTCTTTATAACAACAGCTTATCTGGAGAAATCCAAGG
TCTTTGACTGCTCTGCCGCTGGATGTTCTTGATATCTCAAACAATCGGCTCAGTGGAGAT
20 ATTCCTGTAAATGGTTCCTTTTCGCAGTTCACTTCTATGAGTTTGGCCAATAATAATTA
AGGCCGCGACCTGCATCTCCTTCACCATCACCTTCAGGAACGTCTGCAGCAATAGTAGTG
GGAGTTGCTGCGGTGCAGCACTTCTATTTGCGCTTGCTTGGTGGCTGAGAAGAAAACCTG
CAGGGTCACTTTCTTGATGTACCTGCTGAAGAAGACCCAGAGGTTATTTAGGACAATTT
AAAAGGTTCTCCTTGCGTGAAGTGTAGTTGCTACAGAGAAATTTAGCAAAAGAAATGTA
25 TTGGGCAAAGGACGTTTTGGTATATTGTATAAAGGACGTTTAGCTGATGACACTCTAGTG
GCTGTGAAACGGCTAAATGAAGAACGTACCAAGGGTGGGGAACCTGCAGTTTCAAACCGAA
GTTGAGATGATCAGTATGGCCGTTCATAGGAACTTGCTTCGGCTTCGTGGCTTTTGCATG
ACTCCAACCTGAAAGATTACTTGTTTATCCCTACATGGCTAATGGAAGTGTTGCTTCTTGT
TTAAGAGAGCGTCTGAAGGCAATCCAGCCCTTGACTGGCCAAAAGAAAGCATATTGCT
30 CTGGGATCAGCAAGGGGGCTCGCATATTTACACGATCATTGCGACCAAAGATCATTAC
CTGGATGTGAAAGCTGCAATATACTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGAT
TTTGGGCTAGCAAAATTAATGAATTATAACGACTCCCATGTGACAACTGCTGTACGGGGT
ACGATTGGCCATATAGCGCCCGAGTACCTCTCGACAGGAAAATCTTCTGAGAAGACTGAT
GTTTTTGGGTACGGGGTCATGCTTCTCGAGCTCATCACTGGACAAAAGGCTTTTCGATCTT
35 GCTCGGCTTGCAATGATGATGATATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAA
GAGAAGAAGTTGGAAAGCCTTGTGGATGCAGAACTCGAAGGAAAGTACGTGGAAACAGAA
GTGGAGCAGCTGATACAAATGGCTCTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCA
AAGATGTCAGAAGTAGTGAGAATGCTGGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAA
TGGCAAAAGGAGGAGATGCCAATACATGATTTTAACTATCAAGCCTATCCTCATGCTGGC
40 ACTGACTGGCTCATCCCTATTCCAATCCCTTATCGAAAACGATTACCCCTCGGGGCCA

AGATAAccttttagaaaggggtcatttcttgtgggttcttcaacaagtatatatataggtta
gtgaagttgtaagaagcaaaacccacattcacctttgaatatcactactctataa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS12 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as
described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
leucine zipper motif, containing 2 leucine residues, each
15 separated by seven other amino acids. The third domain
contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
20 contains many serine and proline residues, and is likely to
contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
25 function. The eighth domain represents a serine / threonine
protein kinase domain (Schmidt *et al.* 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
30 leucine rich repeat, probably involved in protein / protein
interactions.

MEHGSSRGFI

WLILFLDFVSRVTGKTQV

35

DALIALRSSLSSGDHTNNILQ

SWNATHVT

PCSWFHVTCNTENSVTRL

DLGSANLSGELV

P QLAQLPNLQYLELFNNNITGEI

5 PEELGDLMELVSLDLFANNISGPI

PSSLGKLGKLRFLRLYNNSLSGEI

PRSLTALP LDVLDISNNRLSGDI

PVNGSFSQFTSMRFA NNKLRRPR

10 PASPSPSPSGGTS

AAIVVGVAAGAALLFALAWWL

RRKLQGHFLDVPAAEEDPE

15 VYLGQFKRFSRLRELLVAT

EKFSKRNVLGKGRFGILYKGRLAD

DTLVAVKRLNEERTKGGELQFQ

TEVEMISMAVHRNLLRLRGFCM

20 TPTERLLVYPYMANGSVASCLR

ERPEGNPALDWPKRKHIALGSA

RGLAYLHDHCDQKIIHLDVKAA

NILLDEEFEAVVGDFGLAKLMN

YNDSHVTTAVRGTFIGHIAPEYL

25 STGKSSEKTDVFGYGVMLLELI

TGQKAFDLARLANDDDIMLLDW

VKEVLKEKKLESIVDAELEGKY

VETEVEQLIQMALLCTQSSAME

RPKMSEVVRMLE

30

GDGLAERWEEWQKEEMPIHDFNYQAY

PHAGTDWLIPYSNSLIENDYPSGPR

35

Arabidopsis thaliana RKS13 cDNA

The start codons encoding predicted the methionine residue of the gene product has been indicated by bold capitals. The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

taataaacctctaataataatggcttttgcttttactctgatgacaagttcaaaa**ATGGAA**
10 **CAAAGATCACTCCTTTGCTTCCTTTATCTGCTCCTACTATTCAATTTCACTCTCAGAGTC**
GCTGGAAACGCTGAAGGTGATGCTTTGACTCAGCTGAAAAACAGTTTGTCATCAGGTGAC
CCTGCAAACAATGTACTCCAAAGCTGGGATGCTACTCTTGTTACTCCATGTACTTGGTTT
CATGTTACTTGCAATCCTGAGAATAAAGTTACTCGTGTTGACCTTGGGAATGCAAACTA
TCTGGAAAGTTGGTTCAGAACTTGGTCAGCTTTTAAACTTGCACTACTTGGAGCTTTAT
15 **AGCAATAACATTACAGGGGAGATACCTGAGGAGCTTGGCGACTTGGTGGAAC TAGTAAGC**
TTGGATCTTTACGCAAACAGCATAAGCGGTCCCATCCCTTCGTCTCTTGCGAAACTAGGA
AAACTCCGGTTCTTGCGTCTTAACAACAATAGCTTATCAGGGGAAATCCAATGACTTTG
ACTTCTGTGCAGCTGCAAGTTCTGGATATCTCAAACAATCGGCTCAGTGGAGATATTCCT
GTTAATGGTTCTTTTTTCGCTCTTCACTCCTATCAGTTTTGCGAATAATAGCTTAACGGAT
20 **CTTCCCGAACCTCCGCCTACTTCTACCTCTCCTACGCCACCACCACCTTCAGGGGGGCAA**
ATGACTGCAGCAATAGCAGGGGGAGTTGCTGCAGGTGCAGCACTTCTATTTGCTGTTCCA
GCCATTGCGTTTGCTTGGTGGCTCAGAAGAAAACACAGGACCACTTTTTTGATGTACCT
GCTGAAGAAGACCCAGAGGTTCAATTTAGGACAACCTCAAAGGTTTACCTTGCGTGAAGT
TTAGTTGCTACTGATAACTTTAGCAATAAAAATGTATTGGGTAGAGGTGGTTTTGGTAAA
25 **GTGTATAAAGGACGTTTAGCCGATGGCAATCTAGTGGCTGTCAAAGGCTAAAAGAAGAA**
CGTACCAAGGGTGGGGAACCTGCAGTTTCAAACCGAAGTTGAGATGATCAGTATGGCCGTT
CATAGGAACTTGCTTCGGCTTCGTGGCTTTTGCATGACTCCAACTGAAAGATTACTTGTT
TATCCCTACATGGCTAATGGAAGTGTTGCTTCTTGTTTAAGAGAGCGTCCTGAAGGCAAT
CCAGCACTTGATTGGCCAAAAAGAAAGCATATTGCTCTGGGATCAGCAAGGGGGCTTGCG
30 **TATTTACATGATCATTGCGACCAAAAAATCATTACCGGGATGTTAAAGCTGCTAATATA**
TTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGATTTTGGGCTCGCAAAATTAATGAAT
TATAATGACTCCCATGTGACAACCTGCTGTACGCGGTACAATTGGCCATATAGCGCCCGAG
TACCTCTCGACAGGAAAATCTTCTGAGAAGACTGATGTTTTTGGGTACGGGGTCATGCTT
CTCGAGCTCATCACTGGACAAAAGGCTTTTCGATCTTGCTCGGCTTGCAATGATGATGAT
35 **ATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAAGAGAAGAAGTTGGAAAGCCTTG TG**
GATGCAGAACTCGAAGGAAAGTACGTGGAAACAGAAGTGGAGCAGCTGATACAAATGGCT
CTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCAAGATGTCAGAAGTAGTGAGAATG
CTGGAAGGAGATGGTTTTAGCTGAGAGATGGGAAGAATGGCAAAAGGAGGAGATGCCAATA
CATGATTTTAACTATCAAGCCTATCCTCATGCTGGCACTGACTGGCTCATCCCCTATTCC
40 **AATTCCTTATCGAAAACGATTACCCCTCGGGTCCAAGATAA**ccttttagaaaggtcctt

ttcttggtgggttcttcaacaagtatatatatagattggtgaagttttaagatgcaaaaaa
aa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS13 protein.

Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains
leucine zipper motifs, containing 2 times 2 leucine residues,
each separated by seven other amino acids. The third domain
15 contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
contains many serine and proline residues, and is likely to
20 contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
function. The eighth domain represents a serine / threonine
25 protein kinase domain (Schmidt et al. 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
leucine rich repeat, probably involved in protein / protein
30 interactions.

MEQRSLLCFLYLL
LLFNFTLRVAGNAEG

35 DALTQLKNSLSSGDP
ANNVLQSWDATLVT

PCTWFHVTCNPENKVTRV

DLGNAKLSGKLV

P ELGQLLNLOYLELYSNNITGEI

PEELGDLVELVSLDLYANSISGPI

5 PSSLGKLGKLRFLRLNNSLSGEI

PMTLTSVQLQV LDISNNRLSGDI

PVNGSFSLFTPISFANNSLTDLPE

PPPTSTSPTPPPPSG

10

GQMTAAIAGGVAAGAAL

LFAVPAIAFAWWL

RRKPQDHFFDVPGAEEDPE

15

VHLGQLKRFTLRELLVAT

DNFSNKNVLGRGGFGKVYKGR LAD

GNLVAVKRLKEERTKGGELQFQ

TEVEMISMAVHRNLLRLRGFCM

20

TPTERLLVYPYMANGSVASCLR

ERPEGNPALDWPKRKHIALGSA

RGLAYLHDHCDQKIIHRDVKAA

NILLDEEFEAVVGDFGLAKLMN

YNDSHVTTAVRG TIGHIAPEYL

25

STGKSSEKTDVFGYGVMLLELI

TGQKAFDLARLANDDDIMLLDW

VKEVLKEKKLESIVDAELEGKY

VETEVEQLIQMALLCTQSSAME

RPKMSEVVRMLE

30

GDGLAERWEEWQKEEMPIHDFNYQA

YPHAGTDWLIPYSNSLIENDYPSGPR

35

Arabidopsis thaliana RKS14 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctgcaccttagagattaataactctcaagaaaaacaagttttgattcggacaaag**ATG**TTG
CAAGGAAGAAGAGAAGCAAAAAAGAGTTATGCTTTGTTCTCTTCAACTTTCTTCTTCTTC
TTTATCTGTTTTCTTTCTTCTTCTTCTGCGAACTCACAGACAAAGTTGTTGCCCTTAATA
GGAATCAAAAGCTCACTGACTGATCCTCATGGAGTTCTAATGAATTGGGATGACACAGCA
GTTGATCCATGTAGCTGGAACATGATCACTTGTCTGATGGTTTTGTCATAAGGCTAGAA
15 GCTCCAAGCCAAAACCTTATCAGGAACCTTTTCATCAAGTATTGGAAATTTAACAAATCTT
CAAACGTATACAGGTTATTGCAGAACAATTACATAACAGGAAACATCCCTCATGAGATT
GGGAAATTGATGAAACTCAAAACACTTGATCTCTCTACCAATAAATTCACTGGTCAAATC
CCATTCACTCTTTCTTACTCCAAAAATCTTCACAGGAGGGTTAATAATAACAGCCTGACA
GGAACAATTCTAGCTCATTGGCAAACATGACCCAACTCACTTTTTTGGATTGTGCGTAT
20 AATAAATTGAGTGGACCAGTTCCAAGATCACTTGCCAAAACATTCAATGTTATGGGCAAT
TCTCAGATTTGTCCAACAGGAACCTGAGAAAGACTGTAATGGGACTCAGCCTAAGCCAATG
TCAATCACCTTGAACAGTTCTCAAAGAACTAAAAACCGGAAAATCGCGGTAGTCTTCGGT
GTAAGCTTGACATGTGTTTGCTTGTGATCATTGGCTTTGGTTTTCTTCTTTGGTGGAGA
AGAAGACATAACAAACAAGTATTATTCTTTGACATTAATGAGCAAAACAAGGAAGAAATG
25 TGTCTAGGGAATCTAAGGAGGTTTAATTTCAAAGAACTTCAATCCGCAACTAGTAACTTC
AGCAGCAAGAATCTGGTCGGAAGAGGGTTTGGAAATGTGTATAAAGGTTGTCTTCAT
GATGGAAGTATCATCGCGGTGAAGAGATTAAAGGATATAAACAATGGTGGTGGAGAGGTT
CAGTTTCAGACAGAGCTTGAAATGATAAGCCTTGCCGTCCACCGGAATCTCCTCCGCTTA
TACGGTTTCTGTACTACTTCCCTCTGAACGGCTTCTCGTTTATCCTTACATGTCCAATGGC
30 AGTGTGCTTCTCGTCTCAAAGCTAAACCGGTATTGGATTGGGGCACAAAGAAAGCGAATA
GCATTAGGAGCAGGAAGAGGGTTGCTGTATTTGCATGAGCAATGTGATCCAAAGATCATT
CACCGTGATGTCAAAGCTGCGAACATACTTCTTGACGATTACTTTGAAGCTGTTGTGCGGA
GATTTCCGGTTGGCTAAGCTTTTGGATCATGAGGAGTCGCATGTGACAACCGCCGTGAGA
GGAACAGTGGGTACATTGCACCTGAGTATCTCTCAACAGGACAATCTTCTGAGAAGACA
35 GATGTGTTCCGGTTTCGGGATTCTTCTTCTCGAATTGATTACTGGATTGAGAGCTCTTGAA
TTCGGAAAAGCAGCAAACCAAAGAGGAGCGATACTTGATTGGGTAAAGAACTACAACAA
GAGAAGAAGCTAGAACAGATAGTAGACAAGGATTTGAAGAGCAACTACGATAGAATAGAA
GTGGAAGAAATGGTTCAAGTGGCTTTGCTTTGTACACAGTATCTTCCCATTCACCGTCTCT
AAGATGTCTGAAGTTGTGAGAATGCTTGAAGGCGATGGTCTTGTGAGAAATGGGAAGCT
40 TCTTCTCAGAGAGCAGAAACCAATAGAAGTTACAGTAAACCTAACGAGTTTTCTTCTCTCT

GAACGTTATTTCGGATCTTACAGATGATTCCTCGGTGCTGGTTCAAGCCATGGAGTTATCA
GGTCCAAGATGAcaagagaaactatatgaatggctttgggtttgtaaaaaa

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS14 protein.

Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
leucine zipper motif, containing 3 leucine residues, each
separated by seven other amino acids. The third domain
15 contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
contains many serine and proline residues, and is likely to
20 contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
function. The eight domain represents a serine / threonine
25 protein kinase domain (Schmidt et al. 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
leucine rich repeat, probably involved in protein / protein
30 interactions.

MLQGRREAKKSYALFSSTFF
FFFICFLSSSSAELTDKV

35

VALIGIKSSLTDP
HGVLMNWDDTAVD

PCSWNMITCSDGFVIR

LEAPSQNLSGTLSS

SIGNLTNLQTVYRLLQNNYITGNI

PHEIGKLMKLTLDLSTNNFTGQI

5 PFTLSYSKLNHRRV NNNSLTGTI

PSSLANMTQLTFDLSYNNLSGPV

PRSLAKTFNVMGNSQICPT

GTEKDCNGTQPKPMSITLNSSQR

10 TKNRK

IAVVFGVSLTCVCLLIIGFGFLLWW

RRRHNKQVLFFDINEQNKE

15 EMCLGNLRRFNFKELQSAT

SNFSSKNLVGKGGFGNVYKGCLHD

GSIIAVKRLKDINNGGGEVQFQ

TELEMISLAVHRNLLRLYGFT

20 TSSERLLVYPYMSNGSVA

SRLKAKPVLWDGTRKRIALGAG

RGLLYLHEQCDPKIIHRDVKAA

NILLDDYFEAVVGDFGLAKLLD

HEESHVTTAVRGTVGHIAPEYL

25 STGQSSEKTDVFGFGILLLELI

TGLRALEFGKAANQRGAILDW

VKKLQOEKKLEQIVDKDLKSNY

DRIEVEEMVQVALLCTQYLPIH

RPKMSEVVRMLE

30

GDGLVEKWEASSQRAET

NRSYSKPNEFSSS

ERYSDLTDDSSVLVQAMELSGPR

35

Legends

Figure 1

5

The different domains of the predicted RKS gene product have the following functions:

The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in
10 targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein
15 protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and
20 Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine /. proline rich region. The next domain displays all the characteristics of a single transmembrane
25 domain (<http://genome.cbs.dtu.dk/services/TMHMM/>). At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062). The kinase domain is followed by a domain
30 with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

Figure 2

35

Alignment of the predicted protein sequences of the different RKS gene products from *Arabidopsis thaliana* with alignX, Vector NTI Suite 5.5 resulted in a phylogenetic tree in which

the relative homology between the different RKS members is shown.

Figure 3

5 Intron-Exon boundaries of the genomic regions on the chromosomes of *Arabidopsis thaliana* encoding the different RKS gene products. Exons are shown as boxes, whereas intron sequences are shown as lines. Sequences encoding LRR domains are displayed in gray colour, transmembrane regions in black.

10

Figure 4.

Cromosomal location of RKS genes in *Arabidopsis thaliana*, showing colocalisation with GASA genes.

15 Figure 5. A signaling complex comprising molecules of RKS proteins, ELS proteins, NDR/NHL proteins and SBP/SPL proteins.

Figure 6.

20 Second generation (T2) tobacco seedlings germinated on MS medium. Transformations were performed with DNA clone 2212-15, representing the overexpression construct GT-RKS4-s. T2 seedlings derived from T1 plant 15.7 shows co-suppression effects while T1 plant 15.6 shows no obvious changes in level of RKS4. T1 plants 15.9 and 15.3 show overexpression effects.
25 Plant 15.7 has the lowest remaining level of RKS4 gene product, whereas plant 15.3 has the highest level of RKS4 gene product.

Figure 7

30 Second generation (T2) tobacco plants. In the upper row the offspring from a co-suppressing T1 plant 15.7 is shown. The middle row shows plants derived from a transgenic T1 plant 15.6 with no clear changes in level of RKS4 is shown while the bottom row shows plants derived from a T1 plant 15.3 in which
35 the levels of RKS4 are increased by the introduction of the overexpression construct GT-RKS4-s.

Figure 8

Second generation (T2) tobacco plants. Plants derived from a co-suppressing T1 plant 15.7 show a reduction in plant size and a delay in the initiation and outgrowth of primordia. The control empty vector transgenic plants show no visible differences in growth compared with the offspring from the transgenic 15.6 plant, in which the endogenous level of RKS4 gene product was not changed. In the overexpressing plants 15.9 and 15.3 organ size was increased, similar as the number of initiated leaf primordia.

Figure 9

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (right picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia is decreased in the transgenic antisense plant compared with the wildtype control.

Figure 10.

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (bottom left picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The upper right picture shows a wildtype flower of the same age as the transgenic antisense flower, grown under similar growth conditions. Total flower size is only slightly decreased in the transgenic antisense flower compared with the control flower, whereas organ size of petals is strongly decreased.

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is increased (upper left picture) due to the presence of a transgenic RKS4 overexpressing construct (GT-RKS4-6s). Compared with the wildtype control flower, total flower size of the transgenic flower is clearly increased. Both sepal and petal organ size is clearly increased compared

with the control.

For comparison an *Arabidopsis thaliana* WS plant is shown which has been transformed with a construct encoding the GAS3 gene in sense direction, i.e. overexpressing GAS3.

5

Figure 11.

Formation of meristematic regions in the hypocotyl of *Arabidopsis thaliana* WS plants under influence of overexpression of RKS4.

10 RKS4 overexpression results in increases in flower and seed organ size that could be due to increase in cell elongation and/or cell division. In order to analyse the cell division patterns in plants with deregulated RKS4 expression the mitotic activity in transgenic plants was analyzed with the a
15 unstable GUS reporter under the control of a cyclin B1;1 promoter (the Plant Journal 1999 (4) 503-508 Spatio-temporal analysis of mitotic activity with a labile cyclin-GUS fusion protein). *Arabidopsis thaliana* WS seedlings with the pCDG construct did not show gus activity (cell division) in
20 hypocotyls (top) whereas the same pCDG line crossed with a constitutive RKS4 construct showed mitotic activity as indicated by GUS-positive cells (bottom); indicating that RKS4 overexpression activated mitotic activity in hypocotyls.

25 Figure 12

In *Arabidopsis thaliana* WS, the seed size is influenced by changing levels of RKS4 gene product. Constitutive overexpression of RKS4 results in increases in seed size (left) compared with control wildtype seeds (right). Antisense
30 constitutive expression of RKS4 cDNA (middle) results in a decrease in seed size compared with the control (right). Magnification is identical in all photos as shown by the bar size.

35

Figure 13

Organ size can be influenced by either modulating cell division or cell elongation or a combination of both. In order to identify the total number of cells and the cell size within an organ the apical site of petals of mature *Arabidopsis* flowers was investigated. Petal organ size is clearly influenced by modulation of RKS4 gene product levels (bottom row for the flowers from which the apical petal epidermal cells were identified). Epidermal cell size is not changed in transgenic plants compared with the control.

Figure 14

Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is increased (right picture) due to the presence of a transgenic RKS10 overexpressing construct. The left picture shows the apical epidermus of a full grown cotyl from an empty vector transgenic seedling of the same age as the transgenic overexpressing cotyl, grown under similar growth conditions..

Figure 15

Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is decreased (right picture) due to the presence of a RKS10 antisense construct The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia remains similar in both the transgenic antisense plants and the wildtype control.

Figure 16

In order to determine organ size variations in transgenic RKS10 transgenic plants compared with empty vector control transgenic plants (pGreen4K), flower organ size was determined of the four open flower stages of *Arabidopsis* inflorescences. The four successive flower stages are photographed under similar magnifications. No obvious changes in organ length could be observed in size of sepals, petals, stamen and carpel

between empty vector control flowers (pGreen4K), flowers with an antisense RKS10 construct (a) or plants overexpressing the RKS10 cDNA under the control of a 35S promoter (S

5 Figure 17

Tissue cultured auxin treated *transgenic Arabidopsis* T2 seedlings were grown on MS agar plates without hormones for a period of 3 weeks. Regeneration potential was scored and the formation and outgrowth of multiple shoot apical meristems from single seedling origin was displayed as (+). The formation and outgrowth of only one shoot apical meristem, leading to the formation of a normal rosette of leaves from individual plants was displayed as (-). Positive regeneration controls consisted of seedlings overexpressing either KNAT1, CUC2, IPT or cycD3. All of these showed an increase of regeneration capacity (+) compared with a negative control GUS overexpressing plant pGreen5K (-). Representative examples of RKS and ELS cDNA overexpressing (s) or antisense (a) cosuppressing constructs in transgenic plants are shown in the bottom panels.

Figure 18.

Tobacco leaf discs were stably transformed with the RKS0 overexpressing construct GT-RKS0-23S and from a single transformation event, large numbers of regeneration plantlets were isolated and subcultured. All of the regenerated plants were potted and flowered. The original transformation event could be kept continuously in tissue culture indefinitely.

30 Figure 19

Seedlings from *transgenic Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown together with a negative control plant (pGreen5K, overexpressing the GUS gene) in which fasciation could never be observed.

Figure 20 - 23

Primary root tips of transgenic *Arabidopsis* plants (top rows) photographed under similar magnification. The bottom rows show the corresponding seedlings (also between each other under the same magnification). Figure 23 shows the specific *Arabidopsis* transgenes with a strong increase in root outgrowth.

Figure 24

Average root length of 10-30 transgenic *Arabidopsis* T2 seedlings from one T1 transgenic plant is shown.

Figure 25

T3 seedlings are shown from a strong co-suppressing RKS10 antisense construct line (T1-4; T2-6; T3 generation) and a strong overexpressing line (T1-4; T2-6; T3 generation). The overexpressing line is different and stronger from the one shown in Figure 4.1-4.5. Pictures are taken under similar magnifications.

Figure 26

T2 seed was germinated on horizontal MS agar plates and pictures were taken under similar magnification of representative examples of the lateral root development from transgenic RKS and ELS transgenic roots.

Figure 27

Pictures taken from transgenic RKS8 or RKS10 overexpressing roots taken directly behind the tip zone. Pictures are taken under same magnification.

Figure 28

Arabidopsis thaliana WS plants in which the endogenous level of RKS or ELS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K).

Overexpression of RKS10 and ELS1 (S) and cosuppression with antisense constructs of RKS8 and also RKS10, result in increased numbers of developing generative meristems.

The generative shoots are photographed with similar magnification.

Figure 29

Arabidopsis thaliana WS plants in which the endogenous level of RKS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K). The top panel shows adult plants under similar magnification. Compared with the control, RKS10 overexpression results in an extreme bushy phenotypic plant. The results of co-suppressing the RKS8 gene product are less dramatic with respect to the bushiness. However, also in these transgenic plants the number of generative meristems is strongly increased compared with the control. The bottom panel shows the generative shoot in detail under similar magnification.

Figure 30

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in transgenic *Arabidopsis* plants containing an antisense (a) RKS10 construct. The terminal flower meristem produces 2 sepals, 1 petal, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. Two new flowers are protruding from this structure, containing all flower organs in normal numbers.

Figure 31

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in transgenic *Arabidopsis* plants T1-11 containing an antisense (a) RKS10 construct. The

terminal flower meristem produces 1 sepal, 2 petals, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. An undetermined flower meristem is protruding from the open carpel structure and forms a number of new flowers, including normal flowers (right) and another abnormal flower (left) which consists of a flower with half of the sepal, petal and stamen organs formed and a new terminal flower meristem protruding from this structure, developing in structures as seen in Figure 7.5. The stamen contain only small numbers of (viable) pollen compared with wildtype stamen (see also chapter 5).

Figure 32

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-11 containing an antisense (a) RKS10 construct (overview shown in Figure 7.4). The terminal flower meristem produces half the normal number of sepals, petals and stamen. The remaining part of the flower structure has converted into a new structure containing a new stem containing a single organ structure resembling a fusion between a petal and a sepal. On this structure several (viable) pollen grains can be observed.

Figure 33

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-12 containing an antisense (a) RKS10 construct. The terminal flower meristem originating from an undetermined generative meristem is here producing an axillary secondary undetermined meristem (left picture), a single organ resembling a stamen (bottom left), a normal flower and a terminal flower. This terminal flower structure contains 2 normal sepals, 2 normal petals, 2 normal stamen (with only a few viable pollen) and two organs resembling a fusion of

sepals /petals/stamen (see also figure 7.7). From this terminal flower structure two new flowers emerge (in a similar fashion as observed in Figure 7.3) containing normal numbers of flower organs (right photos). At the top of this figure a control inflorescence is shown schematically with terminal flower meristems as normally originate from the generative *Arabidopsis thaliana* generative meristem.

Figure 34

Schematic drawing and detailed pictures of several of the structures as shown in figure 7.6. At the right the organs resembling a fusion between sepals/petals/stamen are shown with viable pollen sticking out from these structures. At the top left the single stamen-like organ directly protruding from the main stem is shown.

Figure 35

Transgenic *Arabidopsis* plants overexpressing the RKS13 gene product show a modification of the normal flower inflorescence architecture, somewhat resembling the structures observed in RKS10 antisense plants. A terminal flower containing a normal seed developing silique and a small number of sepals, petals and stamen, develops at least 4 additional terminal flower meristems that develop abnormally themselves, resulting in open carpel structures and modifications of organ structures.

Figure 36

Transgenic plants in which the RKS and / or ELS genes are introduced behind a constitutive 35S promoter in an overexpressing (S) or antisense (a) configuration are analyzed for sterility and characterized further for defects in proper pollen development. As a negative control the normal pollen development of a transgene containing the empty expression vector (pG4K) was included. First generation transgenic flowers of RKS10 expressing constructs and second generation control vector and ELS2 are shown under similar magnification. In detail the stigmatic surface and surrounding stamen, are

shown under similar magnification, showing the presence or absence of pollen on the stamen or the stigmatic surface.

Detailed description

1.Modifying organ size

5

Plant size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth, proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase:

- the size of plant organs
- the growth rate
- the yield of harvested crop
- the yield of total plant material
- the total plant size

Decreasing the levels of endogenous RKS gene product is provided in order to decrease:

- the size of plant organs

the growth rate
the total plant size

5

Results obtained (see also figures 6 to 13)

Overexpression and antisense constructs of full length RKS
cDNA clones have been made under the control of 35S
promoters. Transgenic plants have been produced in *Arabidopsis*
10 *thaliana* and in *Nicotiana tabacum*. Subsequent generations of
stably transformed plants were investigated for phenotypes and
analyzed in detail. The phenotype observed in transgenic
plants with antisense constructs of RKS4 (GT-RKS4-a) could be
described as dwarf plants in which all plant organs showed a
15 decrease in organs size and growth rate. Overexpression of
RKS4 (GT-RKS4-s) resulted in plants with increased size of
organs and an increase in growth rate. Since cell size alone
was not responsible for the modifications in organ size of
petals it can be concluded that RKS4 is involved in the
20 regulation of the cellular divisions during plant growth and
organ formation. Overexpression of RKS 4 results in an
increase of cellular divisions whereas a decrease in
endogenous RKS 4 gene product levels within the plant results
in a decrease of cellular division rates.

25

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2. Cell division

The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes, especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

Possible Applications

Elevation of the levels of the regulating RKS signaling complex members in plant cells in order to increase:

- the size of plant organs
- the growth rate
- the yield of harvested crop
- the yield of total plant material
- the total plant size

Decreasing the levels of endogenous RKS signaling complex members in order to decrease:

the size of plant organs

5 the growth rate

the total plant size

Results obtained

Overexpression and antisense constructs of full length RKS
10 cDNA clones have been made under the control of 35S
promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.

15 Overexpression of RKS 4 results in an increase of cellular divisions whereas a decrease in endogenous RKS 4 gene product levels within the plant results in a decrease of cellular division. Another example of RKS genes involved in cellular proliferation is provided by RKS10. Overexpression of RKS10
20 (S) results in a decrease in apical epidermal cells (Figure 14) compared with control plants containing an empty expression cassette (pGreen4K). Co-suppressing the endogenous RKS 10 gene in plants containing an antisense construct (a) showed clearly larger epidermal cells as the corresponding
25 cells in wildtype control plants (Figure 15). In contrast to the plant phenotypes shown in RKS4 transgenic plants, no differences in plant or organ size could be observed in the RKS10 transgenic plants or organs. This shows that although the organ size remains constant, the number of cells within
30 these organs is variable due to the differences in size of individual cells. These results indicate that normal RKS4 function within the plant can be described as an activator of cellular division.

Normal RKS10 function also involves an activation process on
35 cellular division rate. This effect is also detectable in the root in the region directly behind the tip zone, where in the RKS10 overexpressing transgenes cellular divisions were

detectable in a region where normally cell proliferation has
ceased. The plane of divisions of root cells in these
transgenes is also clearly different from the normal plane of
root cell division, resulting in clumps of cells with all
5 types of division planes possible.

In contrast to RKS4, the final organ size in RKS10 transgenic
plants is under the control of other organ size restriction
processes, in such a way that the final organ volume remains
constant (Figure 16). RKS4 and RKS10 are essentially involved
10 in the same cell cycle activation process, but either addition
organ size controlling functions of these RKS genes or the
hierarchical order in which they regulate the cell cycle is
different.

15

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3. Regeneration

Modification the levels of different RKS and ELS genes within
5 plants allows the initiation and / or outgrowth of apical
meristems, resulting in the formation of large numbers of
plantlets from a single source. A number of gene products that
is able to increase the regeneration potential of plants is
known already. Examples of these are KNAT1, cycD3, CUC2 and
10 IPT. Here we show that modulation of the endogenous levels of
RKS genes results in the formation of new shoots and plantlets
in different plant species like *Nicotiana tabacum* and
Arabidopsis thaliana. herewith the invention provides a method
for modulating a developmental pathway of a plant or plant
15 cell comprising modifying a gene or modifying expression of
said gene, wherein said gene is encoding a protein belonging
to a signaling complex comprising RKS protein, ELS protein,
NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein,
allowing modulating apical meristem formation, in particular
20 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or
RKS10 gene or functional equivalent thereof. A direct
application of a method according to the invention is the
stable or transient expression of RKS and ELS genes or gene
products in order to initiate vegetative reproduction.
25 Regeneration can be induced after overexpression of for
example RKS0 and ELS1; or by co-suppression of for example the
endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or
co-suppression of these RKS and ELS gene products can be
either transient, or stable by integration of the
30 corresponding expression cassettes in the plant genome.

Results obtained

Overexpression and antisense constructs of full length RKS and
ELS cDNA clones have been made under the control of 35S
35 promoters. Transgenic plants have been produced in *Arabidopsis*
thaliana and in *Nicotiana tabacum*. Subsequent generations of

stably transformed plants were investigated for phenotypes and analyzed in detail.

T2 transgenic seedlings of *Arabidopsis* were germinated in liquid MS medium supplemented with 1 mg/L 2,4-D for 1 week, followed by extensive washing and plating of the seedlings onto MS agar plates without hormones. Control transgenic seedstocks containing either a negative control vector (pGreen5K); or positive control overexpression constructs of gene products known to increase the regeneration potential (IPT, KNAT1, CUC2 and cycD3) were characterized for regeneration potential together with seedstocks from plants either overexpressing (s) or co-suppressing (a) all RKS and ELS gene products (Figure 17). Overexpression of the ELS1 and RKS0 cDNA clones resulted in an increase of shoot apical meristem formation and outgrowth, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only increased regeneration results are shown). Antisense constructs of RKS3, RKS4, RKS8 and RKS10 also resulted in an increased formation and outgrowth of apical meristems (Figure 17).

T1 generation *Nicotiana tabacum* tissue cultures transformed with ELS and RKS gene products in either overexpression (s) cassettes or antisense co-suppression (a) cassettes allowed the regeneration of indefinite number of offspring plants from a single transformed cell origin (Figure 18). An example is shown for the overexpression of the GT-RKS0-23S construct. The resulting plants obtained from one transformation event in general showed no phenotypes. Only a subset of plants displayed RKS0 overexpression phenotypes (like loss of apical dominance and early flowering).

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4. Fasciation

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs.

Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is

increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a

signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation

of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems as shown in Figure 19.

A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the

responsible RKS encoding DNA sequences under the control of stage or tissue specific promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordiae by regulation of the

process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural

architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type (an example is shown in Figure 19 where the fasciated meristem of a RKS0-7S *Arabidopsis* plant in which endogenous RKS0 gene product

levels have been deregulated clearly terminates in an *Umbelliferae* type inflorescence.

Results obtained

- 5 Overexpression and antisense constructs of full length RKS
cDNA clones have been made under the control of 35S
promoters. Transgenic plants have been produced in *Arabidopsis*
thaliana. Subsequent generations of stably transformed plants
were investigated for phenotypes and analyzed in detail.
- 10 T2 transgenic seedlings of *Arabidopsis* were germinated on MS
agar plates without hormones. Control transgenic seedstocks
containing a negative control vector (pGreen5K) were tested
for their ability to induce fasciation (Overexpression
constructs (s) of RKS0, RKS8 and RKS10 cDNA clones resulted in
15 fasciated plants, whereas antisense constructs (a) of these
cDNA clones did not increase the regeneration potential (only
positive results are shown). Antisense constructs of RKS3
gave also rise to fasciation (Figure 19).

20

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5. Root development

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the

5 number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of

10 root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of the RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene

15 or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular wherein said gene comprises an ELS1, ELS2, RKS1,

20 RKS3, RKS4, RKS6 RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length

25 can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-

30 suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by

35 overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant

hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector pGreen4K (empty expression vector) and / or pGreen5K (a GUS overproducing vector) were included as references for normal root development. Seedlings from transgenic *Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown together with a negative control plant (pGreen4K, containing an expressing cassette without an insert cDNA). Seedlings are germinated and grown on vertically placed MS agar plates.

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6. Apical meristems

All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering.

Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows

the formation of completely new types of flowers and fused fruit structures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

Results obtained

Changing the normal levels of endogenous RKS10 within the plant, either by overexpressing or co-suppressing the RKS10 cDNA, results in an increase in generative meristem development (Figure 28).

Compared with the control empty vector transgenic pGreen4K plants, large number of meristems are initiated at places were normally no meristems initiate and / or develop. A clear example is shown by co-suppressing the RKS8 gene (Figure 29), where many new inflorescence meristems are initiated from the central generative meristem compared with control pGreen4K plants of the same age. This phenotype is even more extreme in RKS10 overexpressing plants where the resulting plants are extremely bushy with very large numbers of generative meristems formed. Inactivation of the endogenous RKS10 gene in *Arabidopsis* results in modification of meristematic identity as can be shown in Figure 30. A determined flower meristem develops into two new normal terminal flower meristems and a number of terminal flower organ primordia. Another example is shown in Figure 31 where meristem determination is switched from a terminal flower meristem, that normally result only in the normal numbers of terminal organ primordia, towards a number of organ primordia, a new undetermined generative meristem that develop into normal flowers or in a new terminal flower meristem with developmental abnormalities. Only half of the terminal flower primordia develop normally while an extra structure arises resembling a new flower stem with a petal/stamen like organ. The few pollen detectable on this structure (Figure 32) were able to pollinate a MS1 (male sterile) *Arabidopsis* flower. Figure 33 shows the meristematic

developmental switch from a terminal flower meristem into a new undetermined generative meristem, that gives rise to a new formation of another undetermined meristem, and several normal and abnormal terminal flowers. The abnormal flowers again show the fusion of different structures, in this case from sepals, petals and stamen together (Figure 34). Surprisingly, directly on the generative stem another structure, resembling a single stamen was detectable. All these data indicate that a decrease in RKS1 expression levels results in switches in the meristematic identity. Meristems can switch forward and backward between developmental stages, indicating that RKS10 is normally involved in regulating the meristematic identity and the developmental order of meristematic development. RKS13 seems to be involved in similar processes, as can be concluded from the switches in flower meristematic outgrowths observed in figure 35. Modification of the expression levels of RKS1 also results in modified meristem identity. Suppression of endogenous RKS1 levels results in a developmental switching of generative meristems towards vegetative meristems, together with other phenotypes (results not shown).

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7. Male sterility

Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with

5 another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses

10 with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10

15 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment,

20 *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is

25 prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

30 Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants

35 were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic plants

containing a negative control vector pGreen4K (empty expression vector) were included as references for normal stamen and pollen development. RKS10 and ELS2 resulted in sterile plants when overexpressed in *Arabidopsis*. Antisense RKS10 plants resulted in a strong reduction in the number of pollen formed (Figure 36). In order to determine whether pollen development itself was the reason for sterility (and not a combination of pollen developmental mutants coupled to either embryo lethals or female gametogenesis defects), reciprocal crosses were performed between sterile transgenic plants and wildtype *Arabidopsis thaliana* WS plants. These results confirmed that the sterile plants with overexpressing RKS10 and ELS2 constructs were male sterile but completely female fertile. No defects could be observed in embryo development from crosses between female transgenic overexpressors and male wildtype pollen (results not shown). Since both antisense and overexpressing constructs of the RKS10 gene showed defects in proper pollen development we conclude that normal levels of endogenous RKS10 gene product are essential for proper pollen formation, outgrowth and differentiation. In the ELS2 overexpressing plants the initiation of pollen grains was not inhibited. However the proper development of pollen grains in full grown viable pollen was clearly inhibited .

Literature

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8. Resistance mechanisms

Two-hybrid interaction experiments have already shown *in vitro* interaction between RKS and NDR0-NHL and members of the SBP/SPL family. Here we show that *in vivo* the individual components of this signalling cascade are regulating identical processes, as based on functional genomics on transgenics plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex.

Here we show a large number of new members of the NDR/NHL gene family and we postulate a function as syntaxins in the pathogen resistance:

15 **At2g27080;**
 MAERVYPADS PPQSGQFSGN FSSGEFPKKP APPPSTYVIQ VPKDQIYRIP PPENAHRFEQ
 LSRKKTNRSN CRCCFCSFLA AVFILIVLAG ISFAVLYLIY RPEAPKYSIE GFSVSGINLN
 STSPISPSFN VTVRSRNGNG KIGVYEEKES SVDVYYNDVD ISNGVMPVFY QPAKNVTIVK
 LVLGSKIQL TSGMRKEMRN EVSKKTVPFK LKIKAPVKIK FGSVKTWTMI VNVD CDVTVD
 20 KLTAPSRIVS RKCSHDVDLW **

At5g21130
 MTVEKPQEMT GDTNSDGFLT NKDVHRIKHP SLDTNDSSSS RYSVDSQKSR IGPPPGTYVI
 KLPKDQIYRV PPENAHRYE YLSRRKTNKS
 25 CCRRCLCYSL SALLIIIVLA AIAFGFFYL
 YQPHKPQFSV SGVSVTGINL TSSSPFSPVI RIKLRSQNVK GKLGLIYKNG NEADVFFNGT
 KLGNGEFTAF KQPAGNVTVI VTVLKGSSVK LKSSSRKELT ESQKKGKVPF GLRIKAPVKF
 KVGSVTTWTM TITVDCKITV DKLTASATVK TENCETGLSL L*

30 **At1g65690**
 MSQHQQIYPV QDPEAATARP TAPLVPRGSS RSEHGDPSKV PLNQRQPQRFV PLAPPKRRS
 CCCRCFCYTF CFLLLLIVAV GASIGILYLV FKPKLPDYSI DRLQLTRFAL NQDSSLTTAF
 NVTITAKNPN EKIGIYYEDG SKITVWYMEH QLSNGSLPKF YQGHENTTVI YVEMTGQTQ
 ASGLRTILEE QQORTGNIPL RIRVNQPV RV KFGKCLKFEV RFLVRCGVFV DSLATNNVIK
 35 IQSSSCKFRL RL*

At5g36970
 MSDHQKIHPV SDPEAPPHPT APLVPRGSSR SEHGDPTKTQ QAAPLDPPRE KKGSR
 CWCRCVCYTLLVLF LLIVIVGAIV GILYLVRFPK FPDYNIDRLQ LTRFQLNQDL
 40 SLSTAFNVTI
 TAKNPNEKIG IYYEDGSKIS VLYMQTRISN GSLPKFYQGH ENTIIILVEM TGFTQNTATSL
 MTTLQEQQRL TGSIPLRIRV TQPVRIKLGK LKLMKVRFLV RCGVSVDLSA ANSVIRVRSS
 NCKYRFRL*

45 **At1g54540**
 MGDQQKIHPV LQMEANKTKT TTPAPGKTVL LPVQRPIPPP VIPSKNRNMC CKIFCWVLSL
 LVIALIALAI AVAVVYFVFH PKLPSYEVNS LRVTNLGINL DLSLSAEFKV EITARNPNEK
 IGIYYEKGGH IGWVYDKTKL CEGPIPRFYQ GHRNVTKLVN ALTGRAQYGN TVLAALQQQ
 QTGRVPLDLK VNAPVAIKLG NLKMKKIRIL GSCKLVVDSL STNNNNINIK SDCSFKAKL*
 50 **At5g06320**

MADLNGAYYG PSIPPPKKVS HSHGRRGGGC GCLGDCLGCC GCCILSVIFN ILITIAVLLG
IAALIIWLIF RPNAIKFHVT DAKLTEFTLD PTNNLRYNLD LNFTIRNPNR RIGVYYDEIE
VRGYGDQRF GMSNNISKFY QGHKNITTVVG TKLVGQQLVL LDGGERKDLN EDVNSQIYRI
DAKLRLKIRF KFGLIKSWRF KPKIKCDLKV PLTSNSTSGF VFQPTKCDVD F**

5

At5g11890

MTDRVFPASK PPTATNGAPP VGSIPPPAP ATVTSNGTTN GMANQKPQVY IPANRPVYRP
QPYSRRHHHQ SRPSCRRICC CCCFWSILII LILALMTAIA ATAMYVIYHP RPPSFSVPSI
RISRVNLTS SDSSVSHLSS FFNFTLISEN PNQHLFSYSYD PFTVTVNSAK SGTMLGNGTV
PAFFSDNGNK TSFHGVIATS TAARELDPE AKHLRSDLTR ARVGYEIMR TKVKMIMGKL
KSEGVEIKVT CEGFEGTIPK GKTPIVATSK KTKCKSDLV KVKWVSF*

10

At1g17620

MTDDRVPAS KPPAIVGGGA PTNPTFPAN KAQLYNANRP AYRPPAGRRR TSHTRG
CCCRCCWTIFVII LLLLVAAAAS AVVYLIYRPQ RPSFTVSELK ISTLNFTSAV
RLTTAISLSV
IARNPNKNVG FIYDVTDITL YKASTGGDD VVIGKGTIAA FSHGKNTTT LRSTIGSPPD
ELDEISAGKL KGDCLKAKKAV AIKIVLNSKV KVKMGALKTP KSGIRVTCEG IKVVAPTGKK
ATTATTSAK CKVDPRFKIW KITF**

20

At3g11650

MGSKQPYLNG AYYGPSIPPP PKAHRSYNSP GFGCCCFSCS GSCLRCCGCC ILSLICNILI
AVAVILGVAA LILWLIFRPN AVKFYVADAN LNRFSFDPNN NLHYSLDLNF TIRNPNQVRG
VYDEFSVSG YYGDQRFSGA NVSSFYQGHK NTTVILTKIE GQNLVVLGDG ARTDLKDDK
SGIYRINAKL RLSVRFKFWF IKSWKLKPKI KCDDLKIPLG SSNSTGGFKF QPVQCDFDLS**

25

At2g22180

MEGPRRPPSA TAPDSDDDKP DDPPSVWHRP TSSLPALPSL DPPSHGSHHW RNHSLNLSPL
PTTSSPPLPP PDSIPELETY VVQVPRDQVY WTPPPEHAKY VEKRSKNPEK NKKKGCSKRL
LWFFIILVIP GFLLGAILI LHFAFNPTLP VFAVERLTVN PSNFEVTLRA ENPTSNGMVR
YMMKNGVVS LTYKNKSLGS GKFPGLSQA SGSDKVNVL NGSTKNAVQ PRGSKQPVVL
MLNMELKAEY EAGPVKRKE VVVTCDEVK GLLDAKKVEI VSENCESEFK N*

30

At5g22870

MCHKPKLELM PMETSPAQPL RRPSLICIF LVILTILFMA AVGFLITWLE TKPKKLYRYT
ENASVQNFNL TNDNHMSATF QFTIQSHNPN HRISVYSSV EIFVKFKDQT LAFDTVEPFH
QPRMNVKQID ETLIAENVAV SKSNGKDLRS QNSLGKIGFE VFVKARVRFK VGIWKSSHRT
AKIKCSHVT SLSQPNKSQN SSCDADI*

35

40

At2g35980

MAAEQPLNGA FYGPSVPPPA PKGYRGRHG RGCGCCLLSL FVKVIISLIV ILGVAALIFW
LIVRPRAIKF HVTDASLTRF DHTSPDNILR YNLALTVPVR NPNKRIGLYY DRIEHAHAYE
GKRFSTITLT PFYQGHKNTT VLTPTFQGN LVIFNAGQSR TLNAERISGV YNIEIKFRLR
VRFKLGDLKF RRIKPKVDCD DLRLPLSTSN GTTTTSTVFP IKCDFDF**

45

At2g46300

MADYQMNPLV QKPPGYRDPN MSSPPPPPPP IQQQPMRKAV PMPTSYPKK KRRSCCRFCC
CCICITLVLF IFLLLVGTAV FYLWFDPKLP TFSLASFRD GFKLADDPDG ASLSATAVAR
VEMKNPNKSL VFYYGNTAVD LSVGSGNDET GMGETTMNGF RQGPKNSTSV KVETTVKNQL
VERGLAKRLA AKFQSKDLVI NVVAKTKVGL GVGGIKIGML AVNLRCGGVS LNKLDTSPPK
CILNTLKWYK IISN*

50

At4g05220

MTPDRTTIPI RTSPVPRAQP MKRHHSASY AHRVRESLST RISKFICAMF
LLVLFFVGVI AFILWLSLRP HRPRFHIQDF

55

VVQGLDQPTG VENARIAFNV TILNPNQHMG VYFDSMEGSI YYKDQRVGLI
PLLNPFFQQP TTTTIVTGTL TGASLTVNSN RWTEFSNDRA QGTVGFRLLDI
VSTIRFKLHR WISKHHRMHA NCNIVVGRDG LILPKFNHKR CPVYFT*

5 **At2g35460**
MANGLNASY GPPIKPPVKT YYSHGRRGSD VCGGICGCFS SCLLCCGGCL VNIICNILIG
VLVCLGVVAL ILWFILRPNV VKFQVTEADL TRFEFDPRSH NLHYNISLNF SIRNPNQRLG
IHYDQLEVRG YYGDQRFSA NMTSFYQGHK NTTVVGTENL GQKLVLLGAG GRRDFREDRR
SGVYRIDVKL RFKLRFKFGF LNSWAVRPKI KCHLKVPLST SSSDERFQFH PTKCHVDL*

10 **At2g27260**
MQDPSRPATG YPYPPYPNP QQQQPPTNGY PNPAAGTAYP YQNHNPYYAP QPNPRAVIIR
RLFIVFTTFL LLLGLILFIF FLIVRPQLPD VNLNSLSVSN FNVSMNQVSG KWDLQLQFRN
PNSKMSLHYE TALCAMYNR VSLSETRLQP FDQGGKQDTV VNATLSVSGT YVDGRLVDSI
15 GKERSVKGNV EFDLRMISYV TFRYGAFFFF RYVTVYCDV AVGVVPSSGE GKMVGSSKRC
KTY**

At4g01410
MGEGEAKAEH AAKADHKNAP SASSTPESYS KEGGGGGGDA RRAICGAIFT ILVILGIAL
20 ILWLVRPHK PRLTVGAAI YDLNFTAPPL ISTSVQFSVL ARNPNRRVSI HYDKLSMYVT
YKQIITPPL PLPPLRLGHK STVVIAPVMG GNGIPVSPEV ANGLKNDEAY GVVLMRVVIF
GRLRWKAGAI KTGRYGFYAR CDVWLRFNPS SNGQVPLLAP STCKVDV*

At5g22200
25 MTGRYCDQHN GYEERRMRMM MRRIAWACLG LIVAVAFVVF LVWAILHPHG PRFVLQDVTI
NDFNVSQPNF LSSNLQVTVS SRNPNDKIGI FYDRLDIYVT YRNQEVTLAR LLPSTYQGH
EVTWSPFLI GSAVPVAPYL SSALNEDLFA GLVLLNIKID GWVRWKVGSW VSGSYRLHVN
CPAFITVTGK LTGTGPAIKY QLVQRCADV *

30 **At1g61760**
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ILWISLQPHR PRVHIRGFSI SGLSRPDGFE TSHISFKITA HNPQNQVGIY YDSMEGSVY
KEKRIGSTKL TNPFYQDPKN TSSIDGALS PAMAVNKDRW MEMERDRNQG KIMFRLKVR
MIRFKVYTWL SKSHKMYASC YIEIGWDGML LSATKDKRCP VYFT*

35 **At3g52470**
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SQPNLLTSNF QVTIASRNP SKIGIYYDRL HVIATYMNQQ ITLRTAIPPT YQGHKEVNVW
SPFVYGTAVP IAPYNSVALG EEKDRGFVGL MIRADGTVRW KVRTLITGKY HIHVRQAFI
40 NLGNKAAGVL VGDNAVKYTL ANKCSNV**

At5g53730
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ADIYSLNLT STHLLNSSV QLTFLSKNPN KKVGIYYDKL LVYAAYRGQQ ITSEASLPPF
45 YQSHEEINLL TAFLQGTELP VAQSGFYQIS RERSTGKIII GMKMDGKLRW KIGTWVSGAY
RFNVNCLAIV AFGMNMTPP LASLQGTCS TTI*

At4g01110
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50 CRVFCCCVCI TVAIVILLI LTVSVFFLYY SPRLPVVRLS SFRVSNFNF SGGKAGDGLSQ
LTAEATARLD FRNPNGKLR YGNVDVAVS VGEDDFETSL GSTKVKGFE KPGNRTVVIV
PIKVKKQQVD DPTVKRLRAD MKSKKLTVKV MAKTGVGLGV GRRKIVTVGV TISCGGVRLO
TLDSKMSKCT IKMLKWYVPI QVKCI*

55 **At2g35960**
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NLSQPNLLTS NFQITIASRN RNSRIGIYYD RLHVIATYRN QQITLRTAIP PTYQGHKEDN
VWSPFVYGNS VPIAPFNAVA LGDEQNRGFV TLIIRADGRV RWKVGTLITG KYHLHVRCQA
FINLADKAAG VHVGENAVKY MLINKCSNVN *

5 **At3g52460**
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PPYPNYPNAP YQQYPYAQAP PASYYGSSYP AQQNPFVYQRP ASSGFVRGIF TGLIVLVLL
CISTTITWLTV LRPQIPLEFSV NNFSVSNFNV TGPVFSQWT ANLTIENQNT KLKGYFDRIQ
GLVYHQNAVG EDEFLATAFF QPVFVETKKS VVIGETLTAG DKEQPKVPSW VVDEMKKERE
10 TGTVTFSLRM AVWVTFKTDG WAARESLKV FCGKLKVGFE GISGNGAVLL PKPLPCVVYV*

At4g09590
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FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQITLASDL PPTYQRHKED
15 SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGQ VRWKVGTLTI GNYHLHVRCQ
AFINQADKAA GVHVGENTVK YTLINKCSVN F*

At2g35970
MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV SIILQPKKPE FILODITVYA
20 FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQITLASDL PPTYQRHKEN
SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGR VRWKVGTLTI GNYHLHVRCQ
AFINQADKAA GVHVGENTVK YTLINKCSVN F*

At3g26350
25 MSHHHHHETN PHFARIPSON PHLKSGGAST SQTSSNQPHI PPIPHPKKSH HKTTQPHPVA
PPGILIKTRG RHRENPIQEP KHSVIPVPLS PEERLPPRKT QNSSKRPLLL SPEDNQOQRP
PPPQAPQRNG GYGSTLPPI PKPSPWRTAP TSPPHRRGP RLPPPSRETN AMTWSAAFCC
AIFWVILILG GLIILIVYLV YRPRSPYVDI SAANLNAAYL DMGFLLNGDL TILANVTNPS
KKSSVEFSYV TFEYLYYNTL IATQYIEPFK VPKKTSMFAN VHLVSSQVQL QATQSRELQR
30 QIETGPVLLN LRGMFHASH IGPLFRYSYK LHTHCSVSLN GPPLGAMRAR RCNTKR*

At3g11660
MKDCENHGHG RRKLIRRIWF SIIFVLFIIF LTILLIWAIL OPSKPRFILO DATVYAFNVS
GNPPNLLTSN FQITLSSRNP NNKIGIYYDR LDVYATYRSQ QITFPTSIPP TYQGHKDVDI
35 WSPFVYGTSV PIAPFNGVSL DTDKDNVVL LIIRADGRVR WKVGTFITGK YHLHVKCPAY
INFGNKANGV IVGDNAVYKT FTTSCSVSV**

At3g44220
MTEKECEHHH DEDEKMRKRI GALVLGFLAA VLFVVFLVWA ILHPHGPRFV
40 LQDATIYAFN VSQPNYLTSN LQVTLLSSRNP NDKIGIFYDR LDIYASYRNO
QVTLATLLPA TYQGHLDVTI WSPFLYGTTV PVAPYFSPAL SQDLTAGMVL
LNIKIDGWVR WKVGTTWVSGR YRLHVNCPAY ITLAGHFSGD GPAVKYQLVQ RCAVDV*

At1g08160
45 MVPPNPAHQP ARRTQPQLQP QSQPRAQPLP GRRMNPVLCI IVALVLLGLL VGLAILITYL
TLRPKRLIYT VEAASVQEFA IGNNDDHINA KFSYVIKSYN PEKHVSRYH SMRISTAHNN
QSAHKNISP FKQRPKNETR IETQLVSHNV ALSKFNARDL RAEKSKGTIE MEVYITARVS
YKTWIFRSRR RTLKAVCTPV MINVTSSSLD GFQVLCCKTR L**

50 **At2g01080**
MPPPPSSSRA GLNGDPIAAQ NQOPYRSYS SSSSASLKGC CCCLFLLFAF LALLVLAVVL
IVILAVKPKK PQFDLQQVAV VYMGISNPSA VLDPTTASLS LTIRMLFTAV NPNKVGIRYG
ESSFTVMYKG MPLGRATVPG FYQDAHSTKN VEATISVDRV NLMQAHAAADL VRDASLNDRV
ELTVRGDVG KIRVMNFDSP GVQVLLPSFL PAFCSLSDLA *

55 **At5g06330**

MTSKDCGSHD SHSSCNRKIV IWTISIILL ILVVILLVWA ILQPSKPRFV LQDATVFNFN
 VSGNPPNLLT SNFOFTLSSR NPNDKIGIYY DRLDVYASYR SQQITLPSPM LTTYQGHKEV
 NVWSPFVGGY SVPVAPYNAF YLDQDHSSGA IMLMLHLDGR VRWKVGSFIT GKYHLHVRCH
 ALINFGSSAA GVIVGKYMLT ETCSVSV*

5

At5g56050

MSKFSPPPPQS QPQPPETPPW ETPSSKWYSP IYTPWRTTPR STQSTPTTTP IALTEVIVSK
 SPLSNQKSPA TPKLDSMEAH PLHETMVLLQ LRTSRINPWI WCGAALCFIF SILLIVFGIA
 TLILYLAVKP RTPVFDISNA KLNTILFESP VYFNGDMLLQ LNFTNPNKKL NVRFENLMVE
 10 LWFADTKIAT QGVLPFSQRN GKTRLEPIRL ISNLVFLPVN HILELRRQVT SNRIAYEIRS
 NFRVKAIFGM IHYSYMLHGI CQLQLSSPPA GGLVYRNCTT KRW*

At3g20600**NDR1**

15 MNNQNEDETEG GRNCTCCLS FIFTAGLTSL FLWLSLRADK PKCSIQNFPI PALGKDPNSR
 DNTTLNFMVR CDNPNKDKGI YYDDVHLNFS TINTTKINSS ALVLVGNYTV PKFYQGHKKK
 AKKWGQVKPL NNQTVLRAVL PNGSAVFRD LKTQVRFKIV FWKTKRYGVE VGADVEVNGD
 GVKAQKKGK MKKSDSSFP LRSFPISVLM NLLVFFAIR*

At3g54200

MSDFSIPDD KKEEEKPATA MLPPPKNAS SMETQSANTG TAKKLRRKRN CKICICFTIL
 LILLIAIVIV ILAFTLFKPK RPTTTIDSVT VDRLOASVNP LLLKVLLNLT LNVDSLKKNP
 NRIGFSYDSS SALLNYRGQV IGEAPLPANR IAARKTVPLN ITLTLMADRL LSETQLLSDV
 20 MAGVIPLNTF VKVTGKVTVL KIFKIKVQSS SSCDLSISVS DRNVT SQHCK YSTKL*

25

At3g20590

non-race specific disease resistance protein, putative

MTKIDPEEEL GRKCTCFEK FIFTTRLGAL ILWLSLRACK PKCSIQNFYI PALSKNLSSR
 DNTTLNFMVR CDNPNKDKGI YYDDVHLTFS TINTTTTNS DLVLVANYTV PKFYQGHKKK
 30 AKKWGQVWPL NNQTVLRAVL PNGSAVFRD LKTHVRFKIV FWKTKWYRRI KVGADVEVNG
 DGVKAQKKGK KTKKSDSSLP LRSSFPIFVL MNLLVFFAIR *

At4g39740

MSHVTATSLA RFTKPVPKPA SSPIVNTKLT TSGGRTAAFM DLSSFRLTVW
 35 DPDTANDSSG KFPWPRFLFF FLTLKTGGSG LNIKPTISAI AQMMNPMTIT
 EMNNQMRHLE QKLLFLPGS LFLRLSTILH YPGECSNRPD PLEHALRRSR
 SLGLDQEEAA KKVIRVGRDS KNDYVNVVEN QAASFLRRCG PSKRIQSVNY
 CKSTRQGHEI PDVKPLFPTG GGTQAPSRSR ARYAVPAILL GFAGFVGFLH
 YNDERAVPR GQASSNSGCG CGSNTTVKGP IIGGPFTLVS TENKIVTEND
 40 FCGKWLLLYF GYSFSPDVGP EQLKMMKAV DKLAILLNPL TFGCLYLYAE
 FDSRILGLTG TASAMRQMAQ EYRVYFKKVQ EDGEDYLVD TSHNMYLINPK
 MEIVRCFGVE YNPDELSQEL LKEVASVSQ*

At1g32270 syntaxin, putative

45 MVRSDNVKFQ VYDAELTHFD LESNNLQYS LSLNLSIRNS KSSIGIHYDR
 FEATVYYMNQ RLGAVPMP LF YLGSKNTMLL RALFEGQTLV LLKGNERKKF
 EDDQKTGVYR IDVKLSINFR VMVLHLVTWP MKPVVRCHLK IPLALGSSNS
 TGGHKKMLLI GQLVKDTSAN LREASETDHR RDVAQSKKIA DAKLAKDFEA
 ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS QEQRVLMESR
 50 RQEI VLLDNE ISLNEARIEA REQGIQEVKH QISEVMEMFK DLAVMVDHGG
 TIDDIDEKID NLRSAQAQ GK SHLVKASNTQ GSNSSLLFSC SLLLFVFLSG
 DLRCRCVCGS ENPRLNPTRR KAWCEEEDEE QRKKQKKKT MSEKRRREEK
 KVNKPNGFVF CVLGHK*

At1g13050

MSHHHYETNP HFVQFSLODQ HQGGPSSSWN SPHHHQIPQA HSVAPPRVKI KTRGRHQTEP
 PETIHESPSS RPLPLRPEEP LPPRHNPNSA RPLQLSPEEQ RPPHRGYGSE PTPWRRAPTR
 PAYQQGPKRT KPMTLPATIC CAILLIVLIL SGLILLLVYL ANRPRSPYFD ISAATLNTAN
 LDMGYVLNGD LAVVNFNFTNP SKKSSVDFSY VMFELYFYNT LIATEHIEPF IVPKGMSMET
 5 SFHLVSSQVQ IQMIQSQDLQ LQLGTGPVLL NLRGTFHARS NLGSLMRYSY WLHTQCSISL
 NTPPAGTMRA RRCNTRK*

At5g45320

MPRLTSRHGT SPFIWCAAI CAIISIVVIV GGIIVFVGYL VIHPRVPIIS
 10 VADAHLDLFLK YDIVGVLOTQ LTIVIRVEND NAKAHALFDE TEFKLSYEGK
 PIAILKAPEF EVVKEKSMFL PYLVQSYPIP LNPTMMQAVD YAVKKDVITF
 ELKGGSRTRW RVGPLGSVKF ECNLSCQLRF RPSDHSYIPS PCTSAHKH*

At3g20610

MDRDDAWEFV VTIVGSLMTL LYVSFLLALC LWLSTLVHHI PRCSIHYFYI PALNKSLISS
 15 DNTTLNFMVR LKNINAKQGI YYEDLHLSFS TRINNSSLV ANYTVPRFYQ GHEKKAKKWG
 QALPFNNQTV IQAVLPNGSA IFRVDLKMV KYKVMWSWTK RYKLGASVNL EVNEDGATKV
 KDKEDGIKMK ISDSSPQRLT FFQVCFSIIC VLMNWLIFLA IR*

At4g26490

MVLTKPATVR FNGLDAPRK DRVILQPRS SRTSLWIWCV AVFLAIRPRI PVFDIPNANL
 20 HTIYFDTPF FNGDLSMLVN FTNPNKKIEV KFEKLRIELF FFNRLIAAQV VQPFLOKKHE
 TRLEPIRLIS SLVGLPVNHA VELRRQLENN KIEYEIRGTF KVKAHFGMIH YSYQLHGRCQ
 LQMTGPPTGI LISRNCTTK *

At5g42860

MHAKTDSEVT SLSASSPTRS PRRPAYFVQS PSRDSHDGEK TATSFHSTPV
 LTSPMGSPPH SHSSSRFSK INGSKRKGHA GEKQFAMIEE EGLLDDGDRE
 QEALPRRCYV LAFIVGFSL FAFSLILYA AAKPQPKIS VKSITFEQLK
 30 VQAGQDAGGI GTDMITMNAT LRMLYRNTGT FFGVHVTSSP IDLSFSQITI
 GSGSIKKFYQ SRKSQRTVVV NVLGDKIPLY GSGSTLVPPP PPAPIPKPKK
 KKGPIVIVEP PAPPAPVPMR LNFTVRSRAY VLGKLVQPKF YKRIVCLINF
 EHKKLSKHIP ITNNCTVTI *

At1g45688

MHAKTDSEVT SLAASSPARS PRRPVYVQS PSRDSHDGEK TATSFHSTPV LSPMGSPPHS
 35 HSSMGRHSRE SSSSRFSGSL KPGSRKVNPN DGSKRKGHGG EKQWKECAVI EEGLLDDGD
 RDGGVPRRCY VLAIVGFSL LFGFSLILY GAAKPMKPKI TVKSITFETL KIQAGQDAGG
 VGTDMITMNA TLRMLYRNTG TFFGVHVTST PIDLSFSQIK IGSGSVKKFY QGRKSERTVL
 40 VHVIGEKIPL YGSGSTLLPP APPAPLPKPK KKGAPVPIP DPPAPPAPV MTLSEFVRSR
 AYVLGKLVQP KFYKKIECDI NFEHKNLNKH IVITKNCTVT TV*

At4g26820

MDDEQNLVEE MNQOLLITVI DTEKVPRLP ISSRSHQESE PANISHWSLL FKLFLAITIM
 45 GACVAGVTFV ILITPTPTV HVQSMHISFA NNLVPWSAT FSIKNPNEKL HVTYENPSVW
 LVHRGKLVST ARADSFQKG GEKNEVIVKR NETKVIDEEA AWEMEDEVAV TGGVVGGLDMV
 FSGRVGFYPG TSALWGEQYM SAVCENVSAK LYNVDDEIYG TNRSVLSFDG RLVCSVRLPK
 YP*

50

Plants respond in a variety of ways to pathogens. After a recognition of the pathogen, normally mediated by avr and R genes, the resulting response induces a hypersensitive

response, that results in inhibition of the pathogen. After the recognition, further processes appear to be non-specific. In addition to the hypersensitive response, a second line of defence, defined as the systemic acquired resistance response can be triggered, that renders unaffected parts of the plant resistant to a variety of normally virulent pathogens. Several of the RKS and ELS gene products prove to be key regulators in the regulation of the system acquired resistance response.

- 10 Overexpression of several of the RKS and / or ELS genes in plants, either by constitutive promoters, stage and / or tissue specific promoters, or inducible promoters allows the activation of a systemic acquired resistance response in plants.
- 15 Another application can be provided by the activation of a RKS /ELS specific ligand in (transgenic) plants, thereby activating the receptor complex, that finally results in triggered activation of the systemic acquired resistance response in these plants.
- 20 (ref. Generation of broad-spectrum disease resistance by overexpression of an essential regulatory gene in systemic acquired resistance. H. Cao et al. 1998. Proc. Natl. Acad. Sci. USA 95: 6531-6536). Recent literature shows the functional interaction between RKS10 and BRI-1, another class
- 25 of transmembrane LRR receptor kinases (Cell Vol. 110, 213-222 2002). BAK1=RKS10 as described here, interacts with BRI-1 and modulates brassinosteroid signaling; Cell vol 110, 203-212 2002 BRI1/BAK1 a receptor kinase pair mediating brassinosteroid signaling). Brassinosteroids are known to
- 30 function in a broad range of disease resistance in tobacco and rice (Plant Journal 2003, 887-898). The BRI-1 receptor is involved in the binding of systemin, an 18 amino acid polypeptide, representing the primary signal for the systemic activation of defence genes (PNAS 2002, 9585-9590).
- 35 ELS overexpression phenotypes mimic the effects of inactivation of RKS molecules gene products. Either ELS is competing for ligand binding, or ELS inhibits the interactions

between RKS and BRI-1-like gene products. ELS1 overexpression results in dwarf phenotypes in Arabidopsis and tobacco plants, similar as observed for antisense RKS4 and RKS10, and for knock out plants of RKS0 and RKS4.

- 5 Deregulating expression of ELS and / or RKS genes in plant would modify the broad spectrum disease resistance in such plants. This would explain the observed data that brassinosteroids are involved in disease resistance (Plant Journal 2003, 33 887-898.)

Further references

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Claims

1. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying
5 expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein or encoding a protein comprising a ligand for said complex.
- 10 2. A method according to claim 1 allowing modulating cellular division during plant growth or organ formation
3. A method according to claim 2 wherein said gene comprises
15 an RKS4 or RKS10 gene or functional equivalent thereof.
4. A method according to claim 1 allowing modulating apical meristem formation.
- 20 5. A method according to claim 4 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof.
6. A method according to claim 4 allowing modulating
25 fasciation.
7. A method according to claim 6 wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof.
- 30 8. A method according to claim 4 allowing modulating root development.
9. A method according to claim 7 wherein said gene comprises
35 an ELS1, ELS 2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof.

10. A method according to claim 4 allowing modulating meristem identity.

11. A method according to claim 9 wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof.

12. A method according to claim 1 allowing modulating pollen development.

13. A method according to claim 11 wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

14. A method for providing resistance to a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising NDR/NHL protein, or encoding a protein comprising a ligand for said complex.

15. A method for obtaining a plant or plant cell with a modulated development comprising subjecting a plant or plant cell to a method according to anyone of claims 1 to 13.

16. A method for obtaining a resistant plant or plant cell comprising subjecting a plant or plant cell to a method according to claim 14.

17. A plant or plant cell obtainable with a method according to claim 15 or 16.

Fig. 1

Different domains of RKS proteins

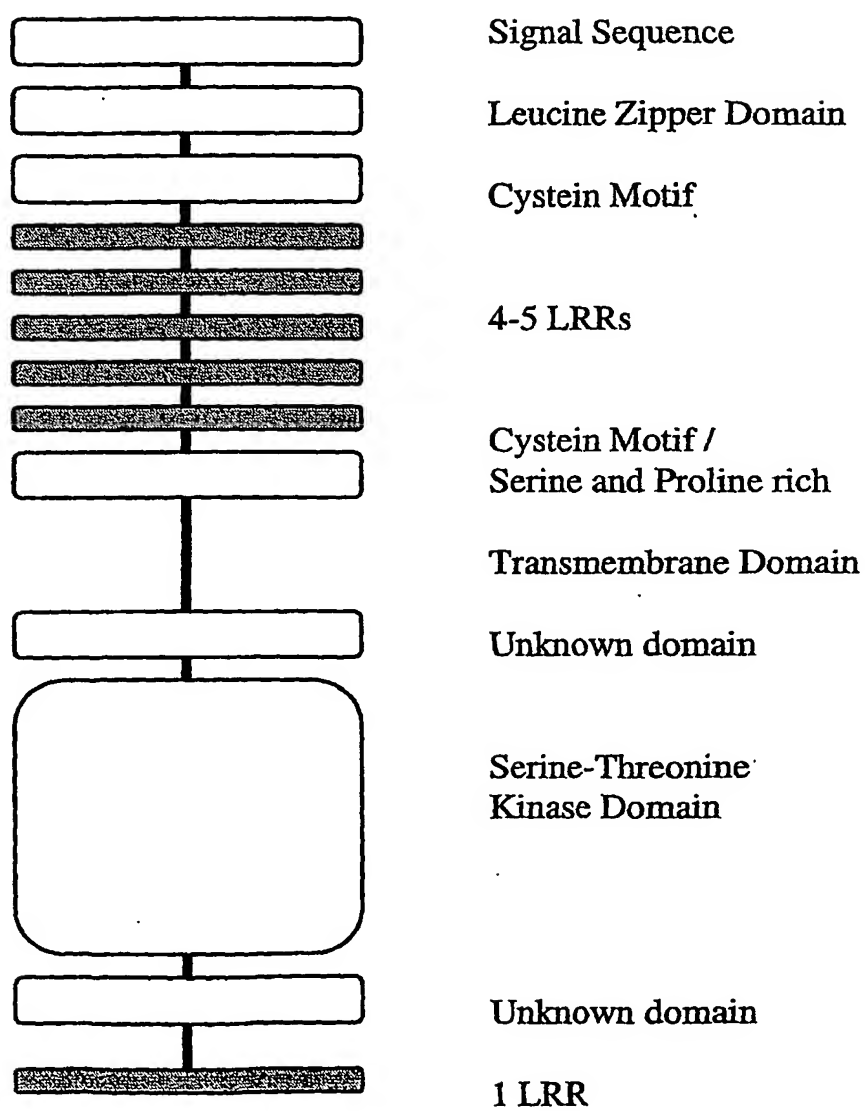


Fig. 2

Developmental tree of the different Receptor Kinases like SERK (RKS) genes.

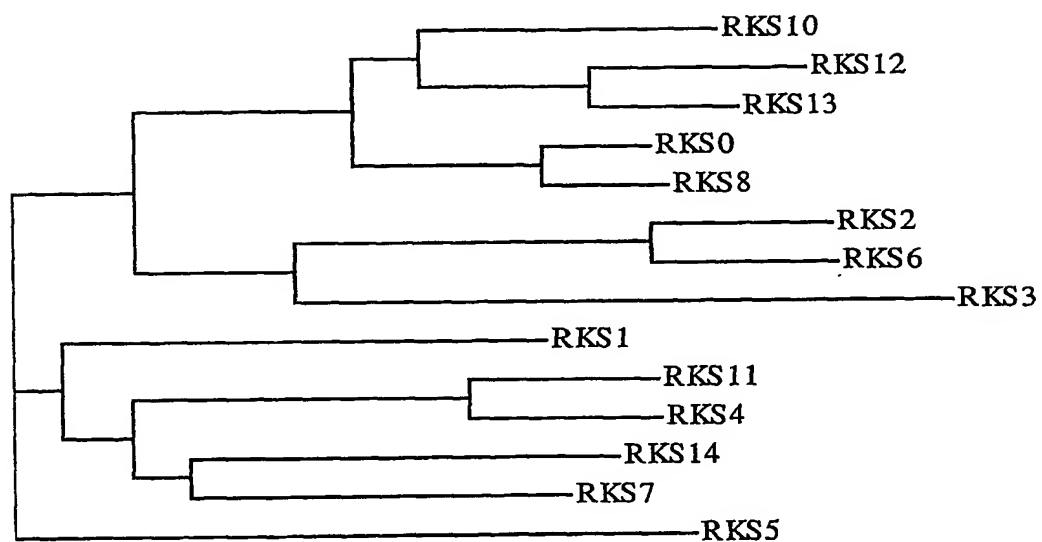
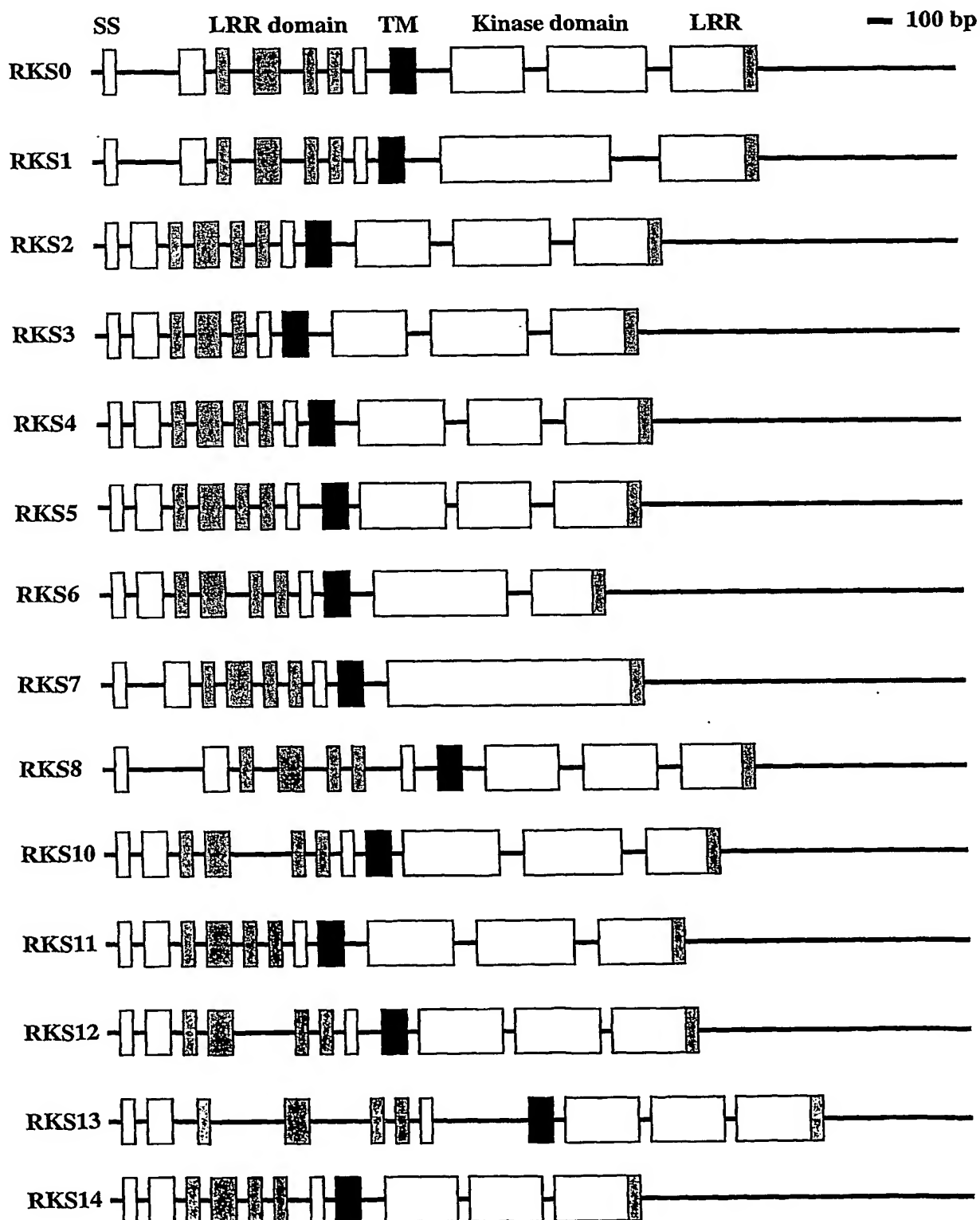


Fig. 3

Intron-Exon structure of the RKS genes in *Arabidopsis thaliana* var. Columbia.
SS signal sequence; LRR leucine rich repeat domain; TM transmembrane domain.



Chromosomal location of RKS genes
in *Arabidopsis thaliana*

I II III IV V

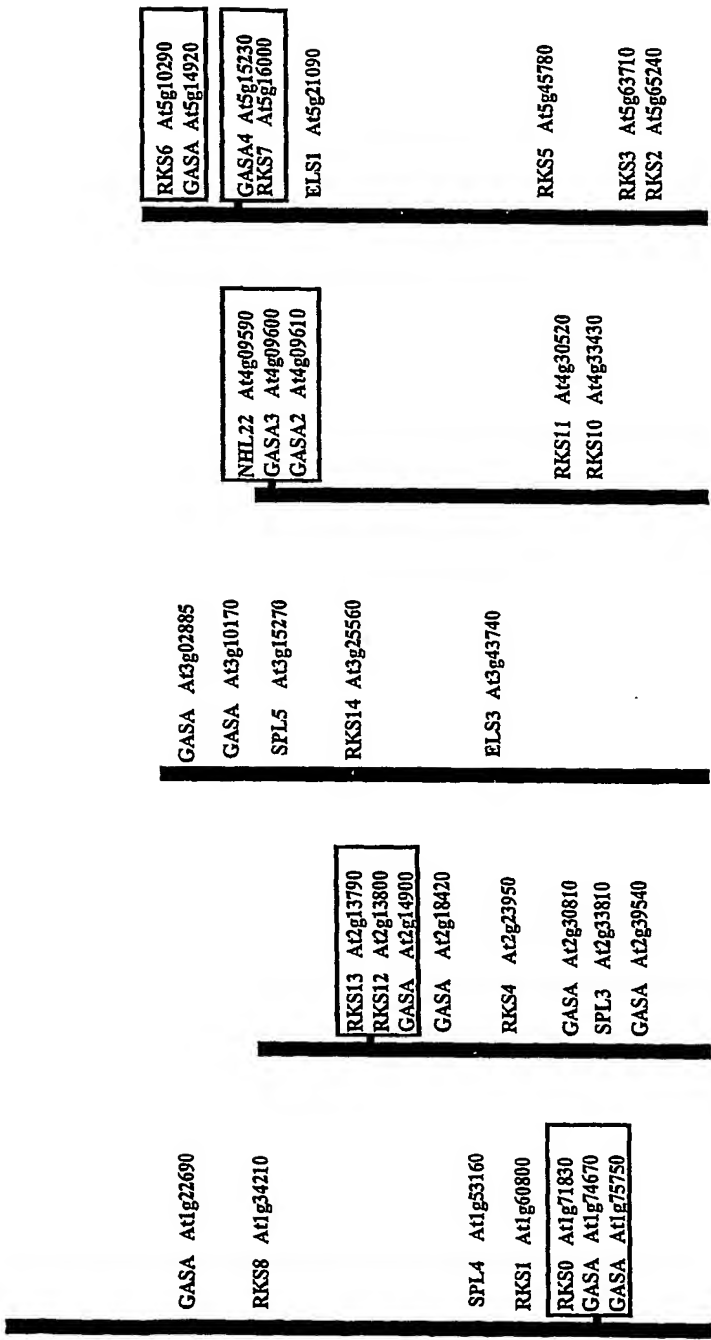


Fig. 4

RKS-mediated signal transduction pathway in plants

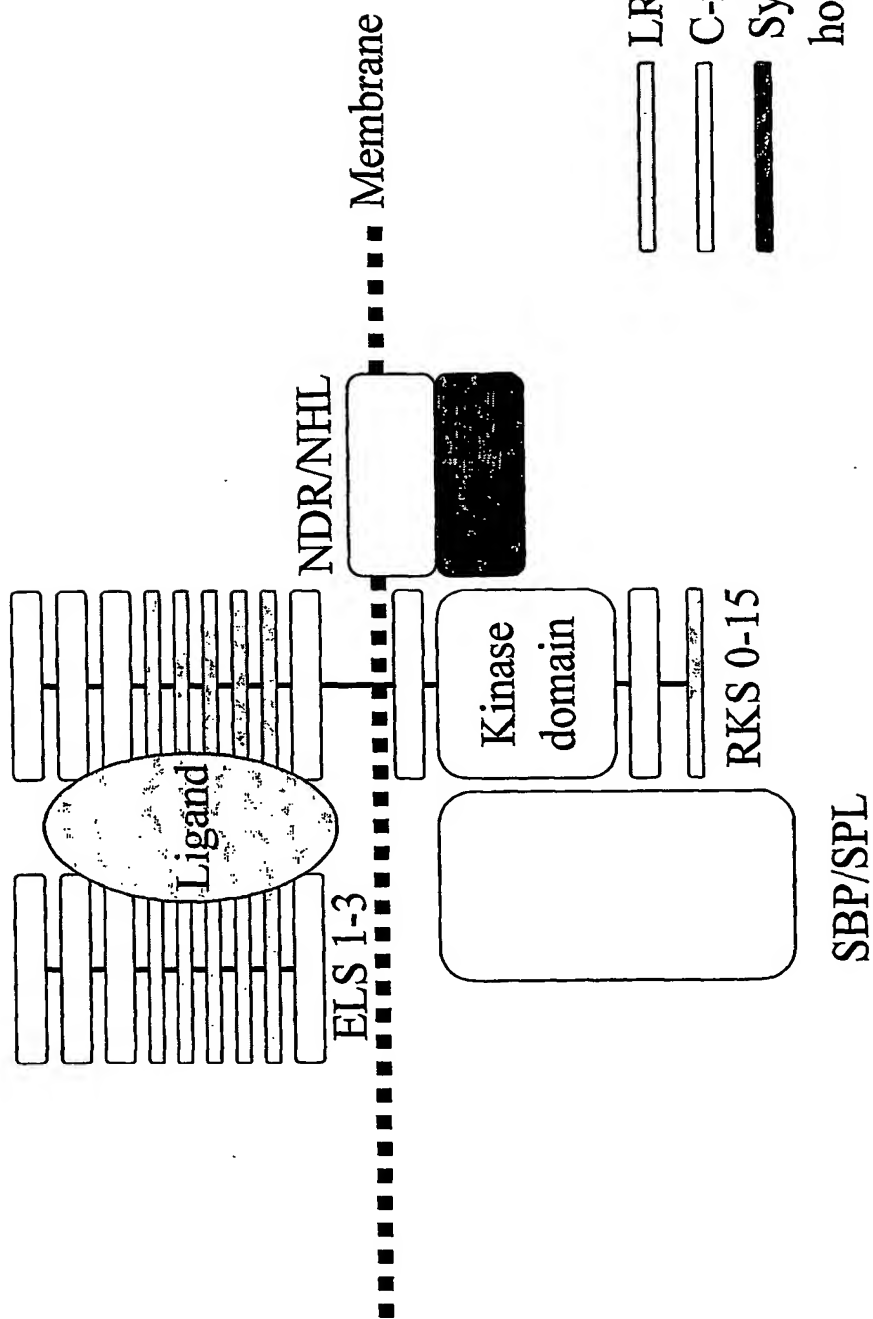
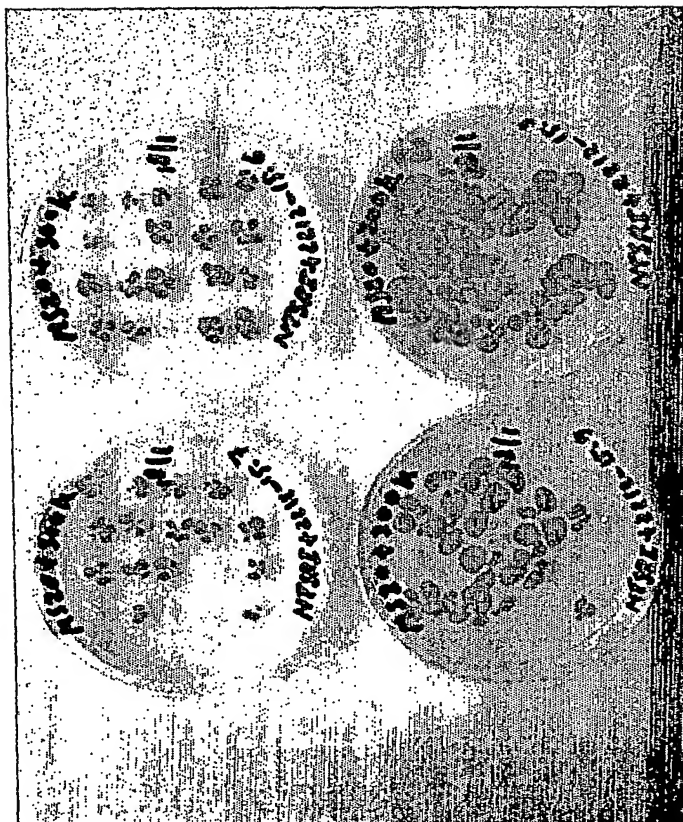


Fig. 5

GT-RKS4 determines seedling size
in *Nicotiana tabacum*.



Modifications in the
expression profile
of GT-RKS4 modulates
organ size within seedlings
of *Nicotiana tabacum*.

Fig. 7

GT-RKS4 determines organ size
in *Nicotiana tabacum*.

GT-RKS4-7S-T2

GT-RKS4-6S-T2

GT-RKS4-3S-T2

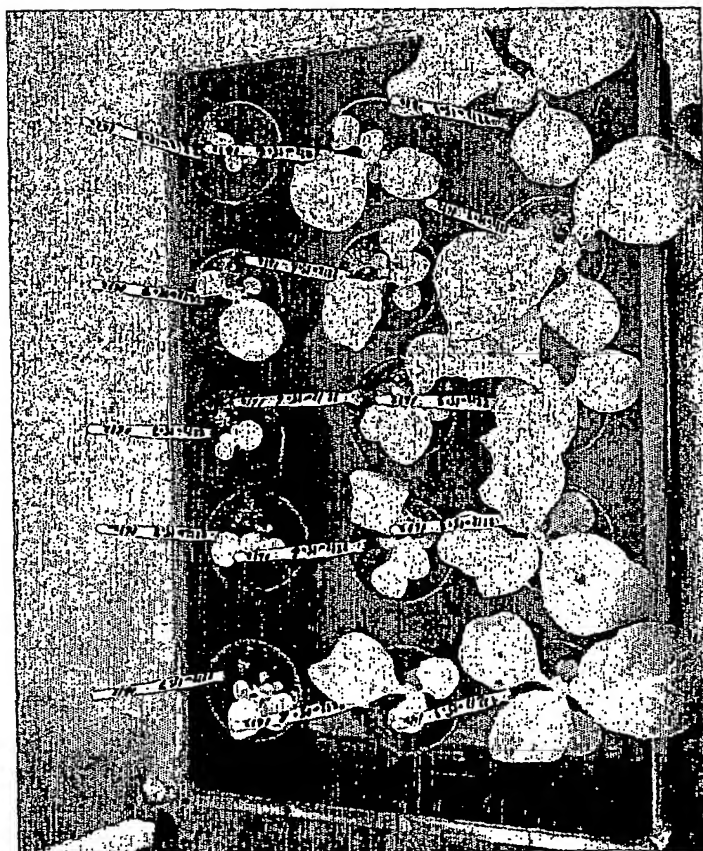
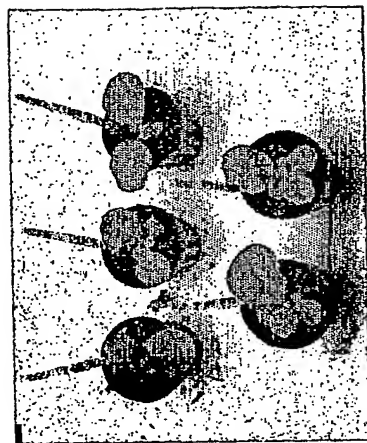
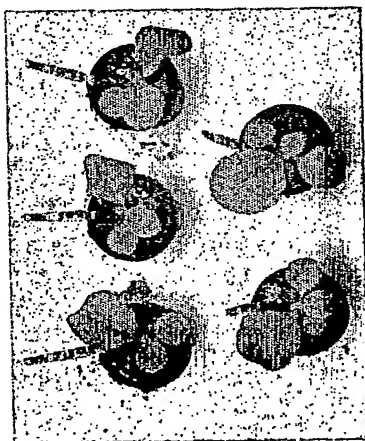


Fig. 8

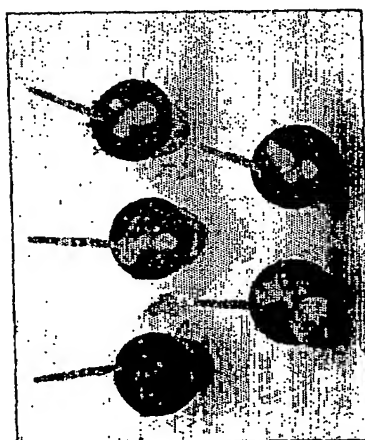
GT-RKS4 determines plant size
in *Nicotiana tabacum*



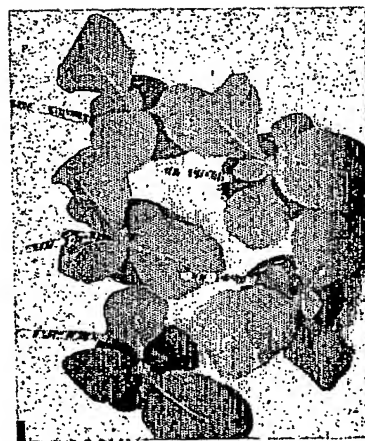
Empty vector control



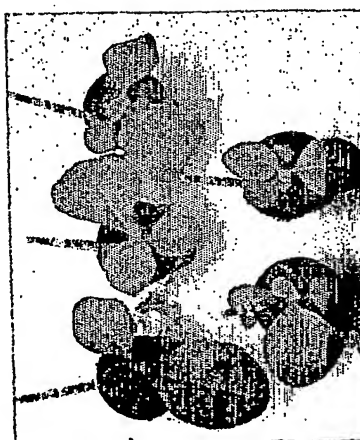
GT-RKS4-15S-6T2



GT-RKS4-15S-7T2



GT-RKS4-15S-3T2

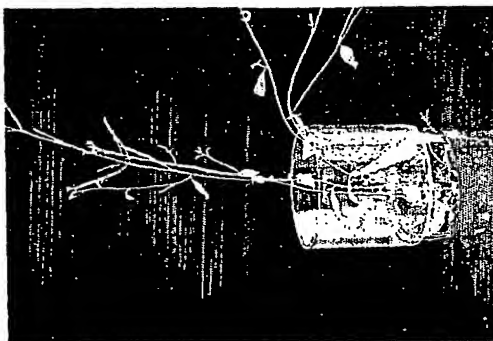


GT-RKS4-15S-9T2

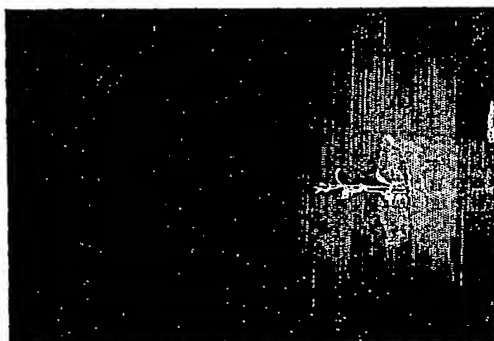
Fig. 9

Stable transformed GT-RKS4-antisense
in *Arabidopsis thaliana*

Wildtype WS



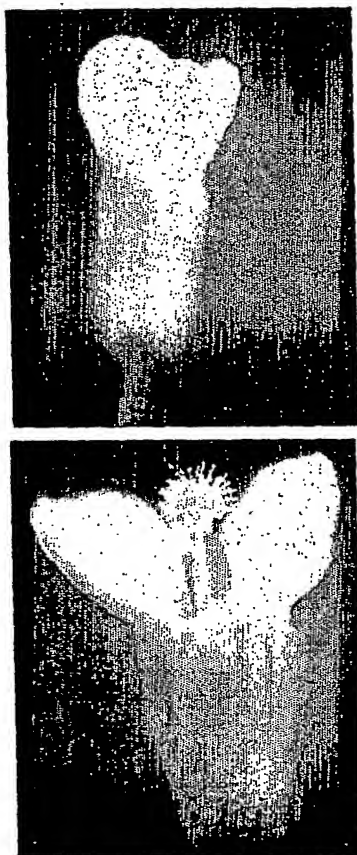
GT-RKS4-16a



Overexpression of antisense GT-RKS4-1a
reduces plant and organ size.

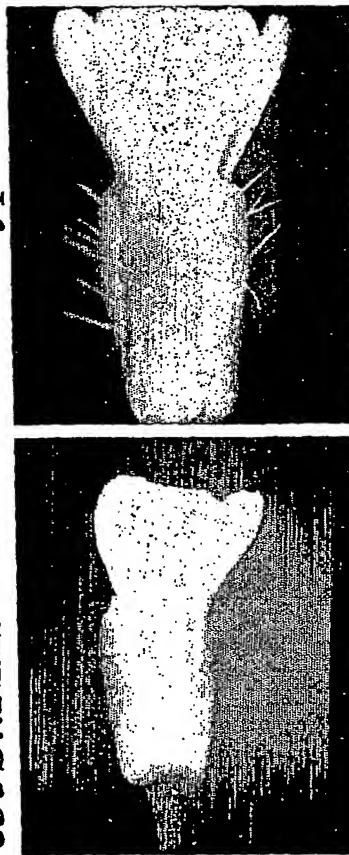
Fig. 10

Ectopic expression of RKS4 and GAS3
gene products both result in increases
flower size in *Arabidopsis thaliana* WS



Wildtype WS

e35S::RKS4 sense

e35S::RKS4
antisense

e35S::GAS3 sense

Fig. 11

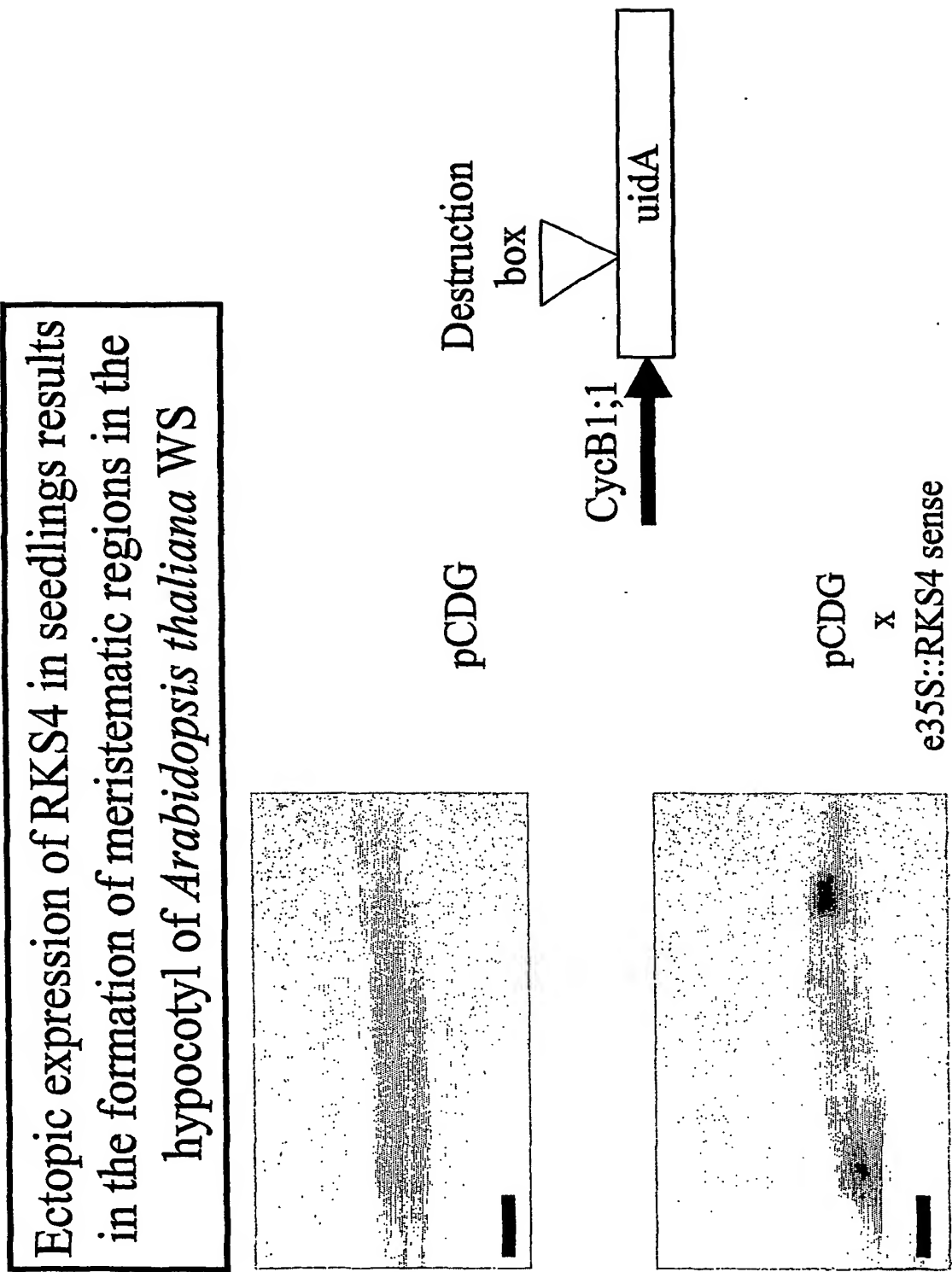


Fig. 12

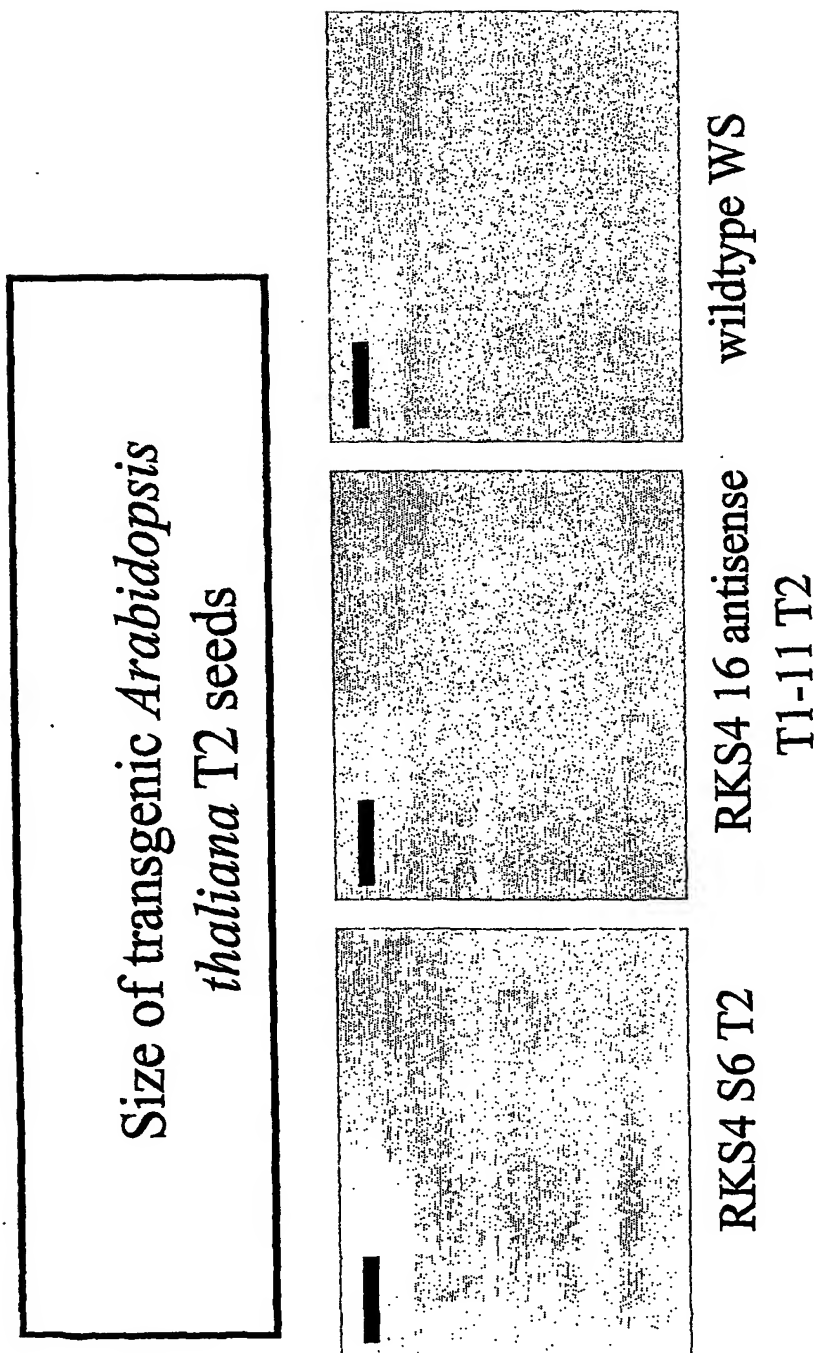


Fig. 13

RKS4 regulates cell number and cell size in *Arabidopsis thaliana*.

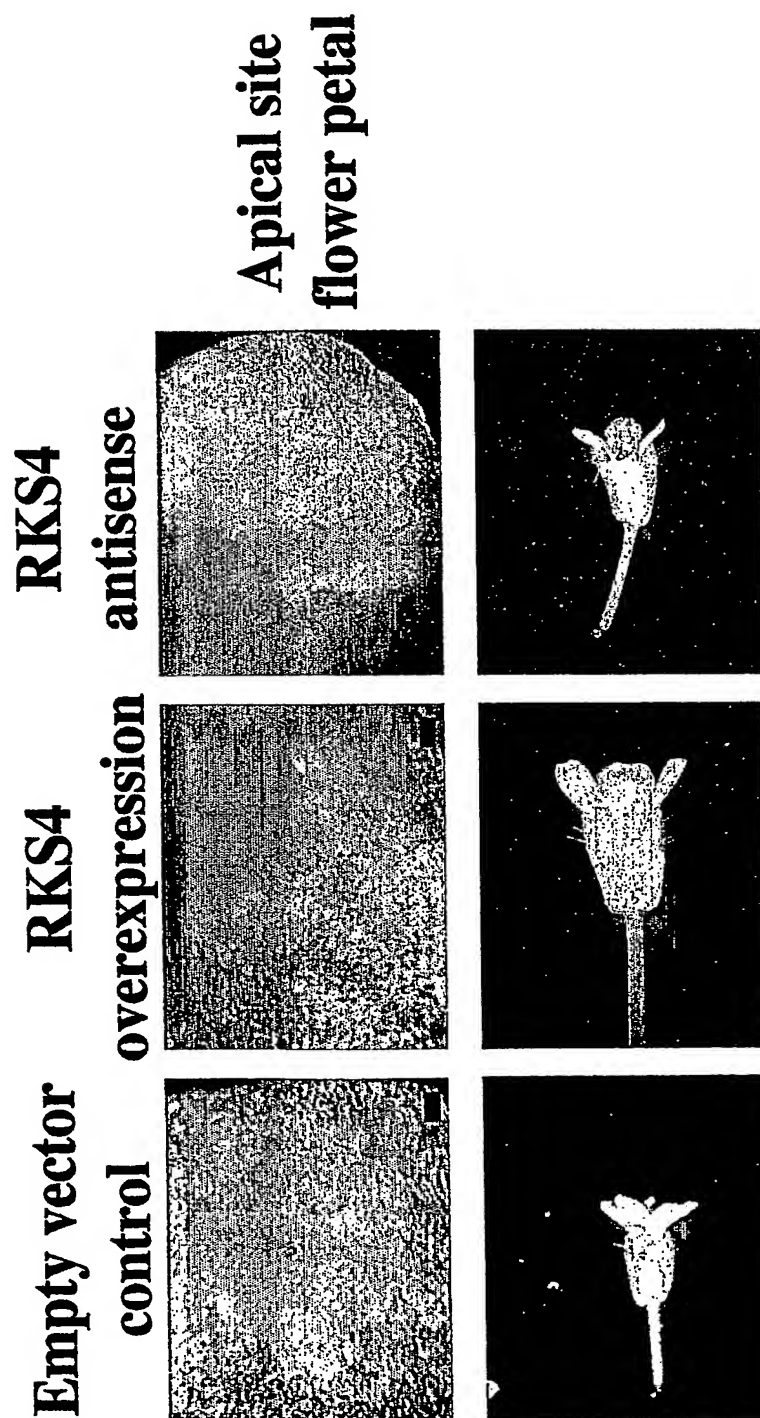
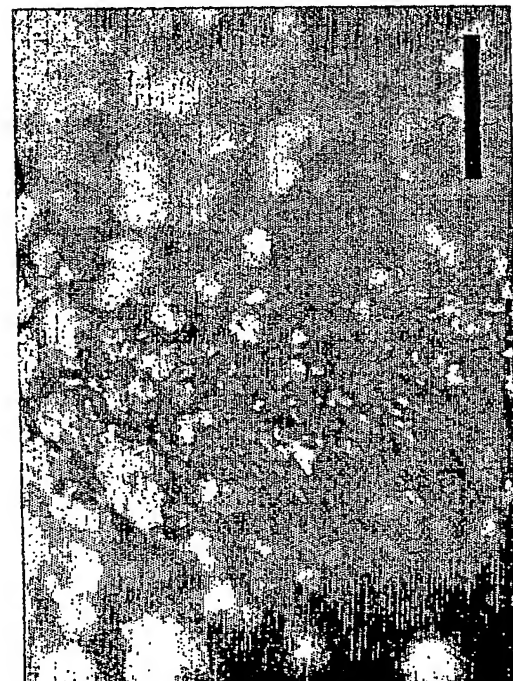
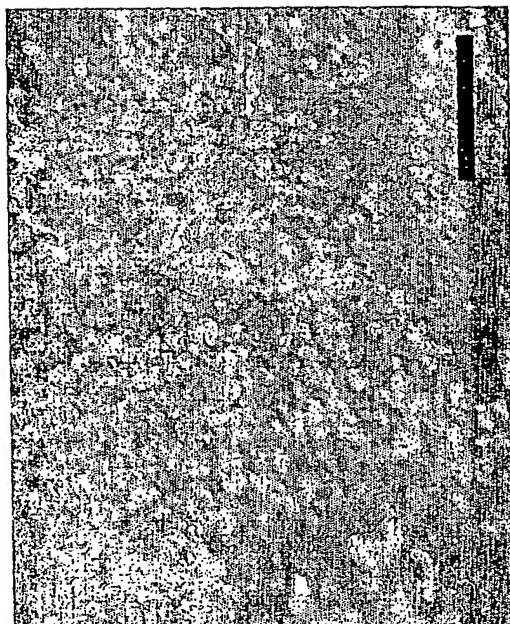


Fig. 14

RKS10S T1-10
results in a decrease in size
of cotyl-like apical epidermal cells



pGreen 4K



RKS10S T1-10

Fig. 15

RKS10antisense T1-4
results in an increase in size
of the cotyl epidermal cells

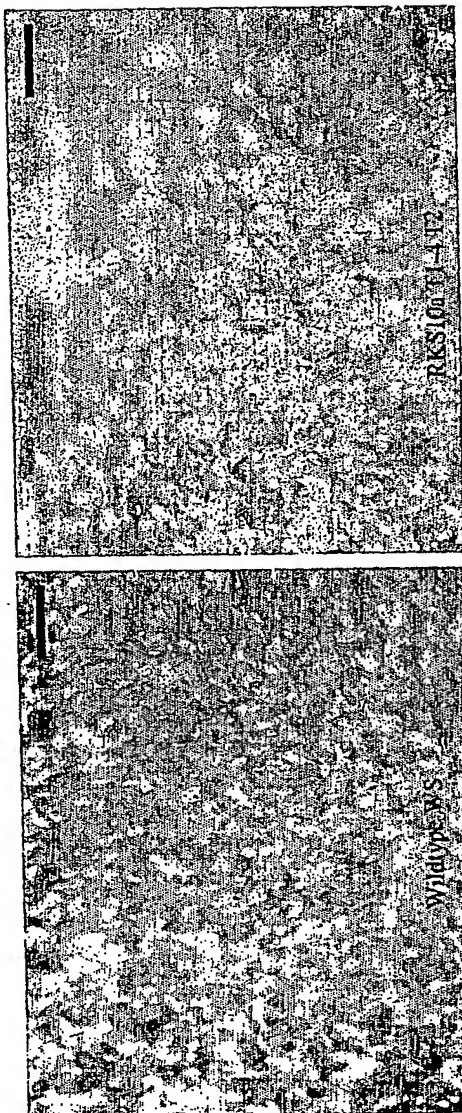


Fig. 16

Flower development from the same
influorescence in transgenic
Arabidopsis thaliana

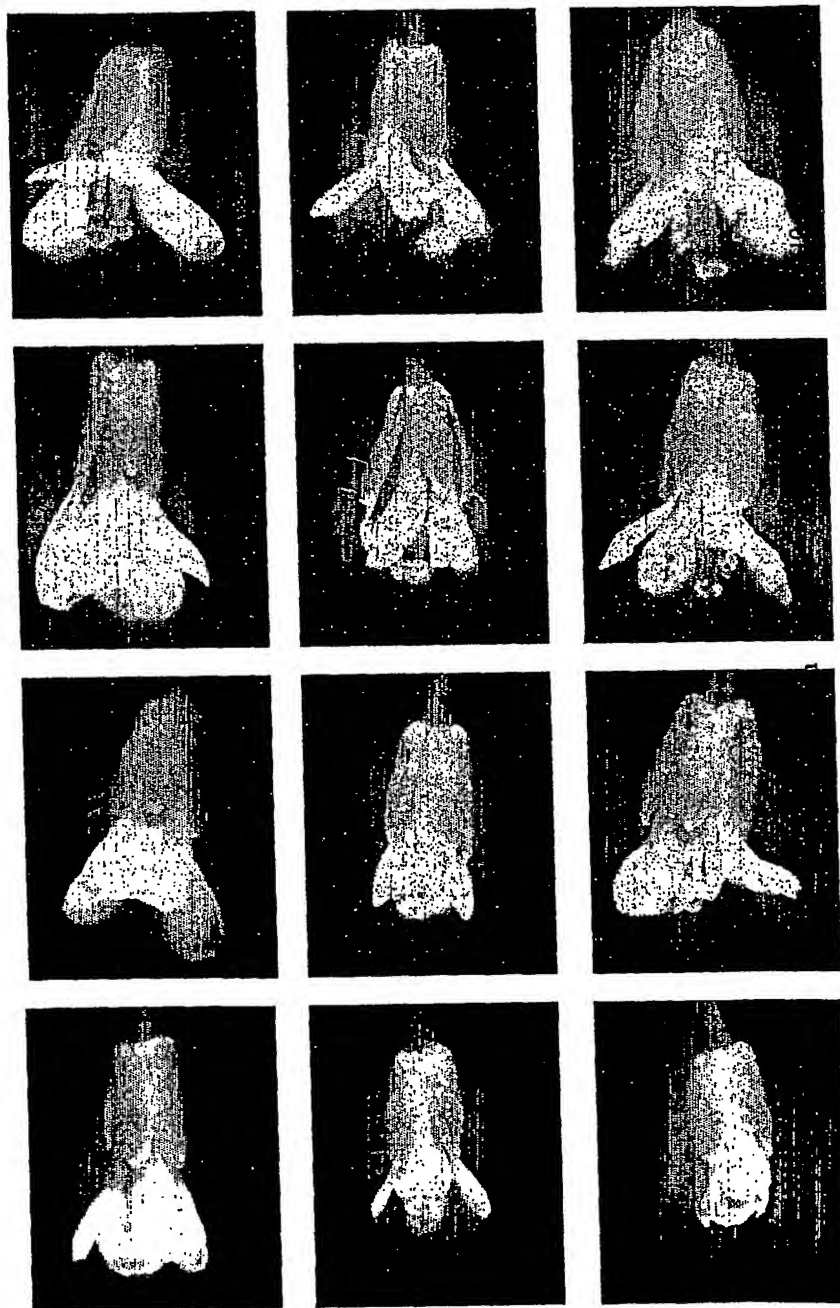


Fig. 17

Regeneration potential of
Arabidopsis transgenic seedlings.

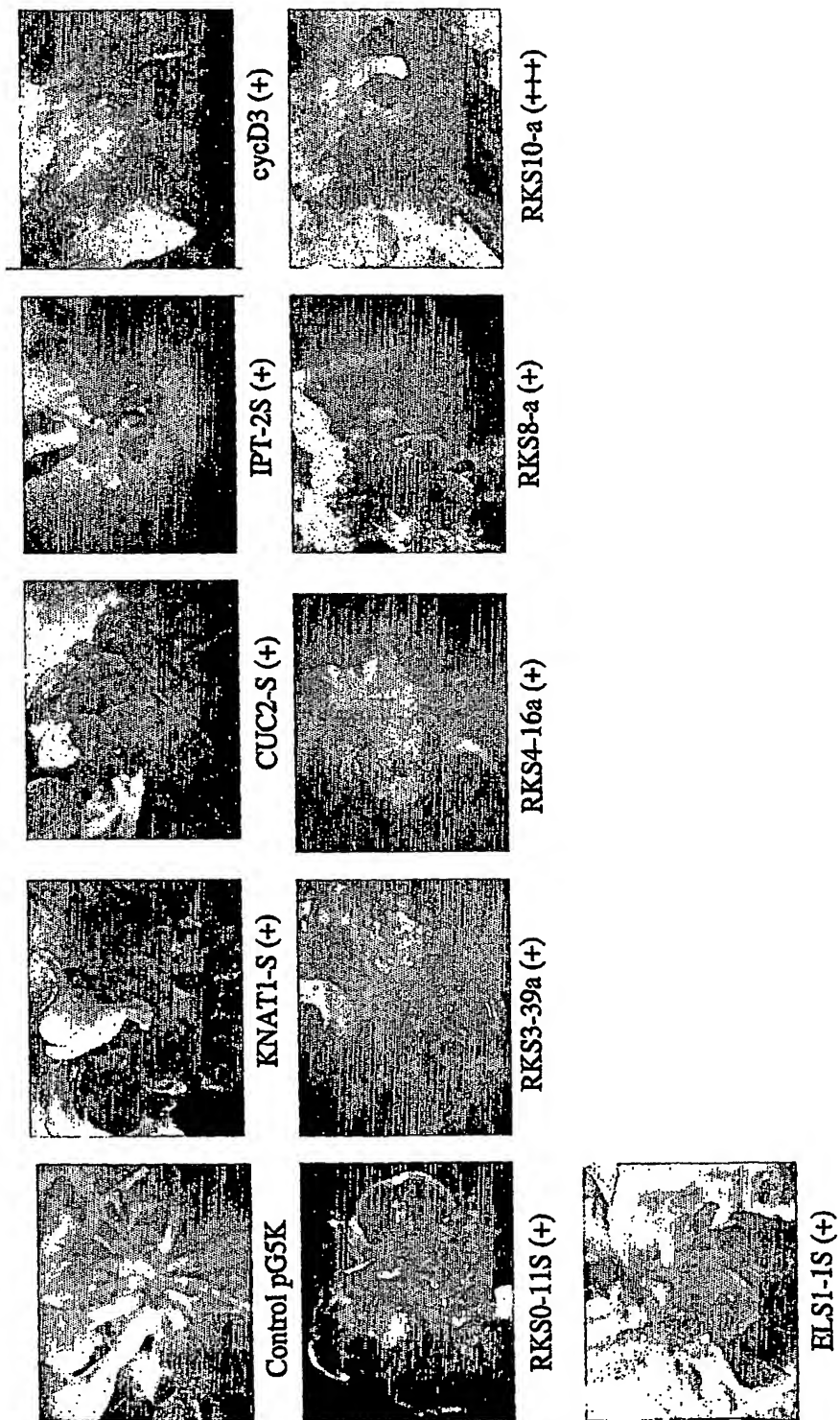


Fig. 18

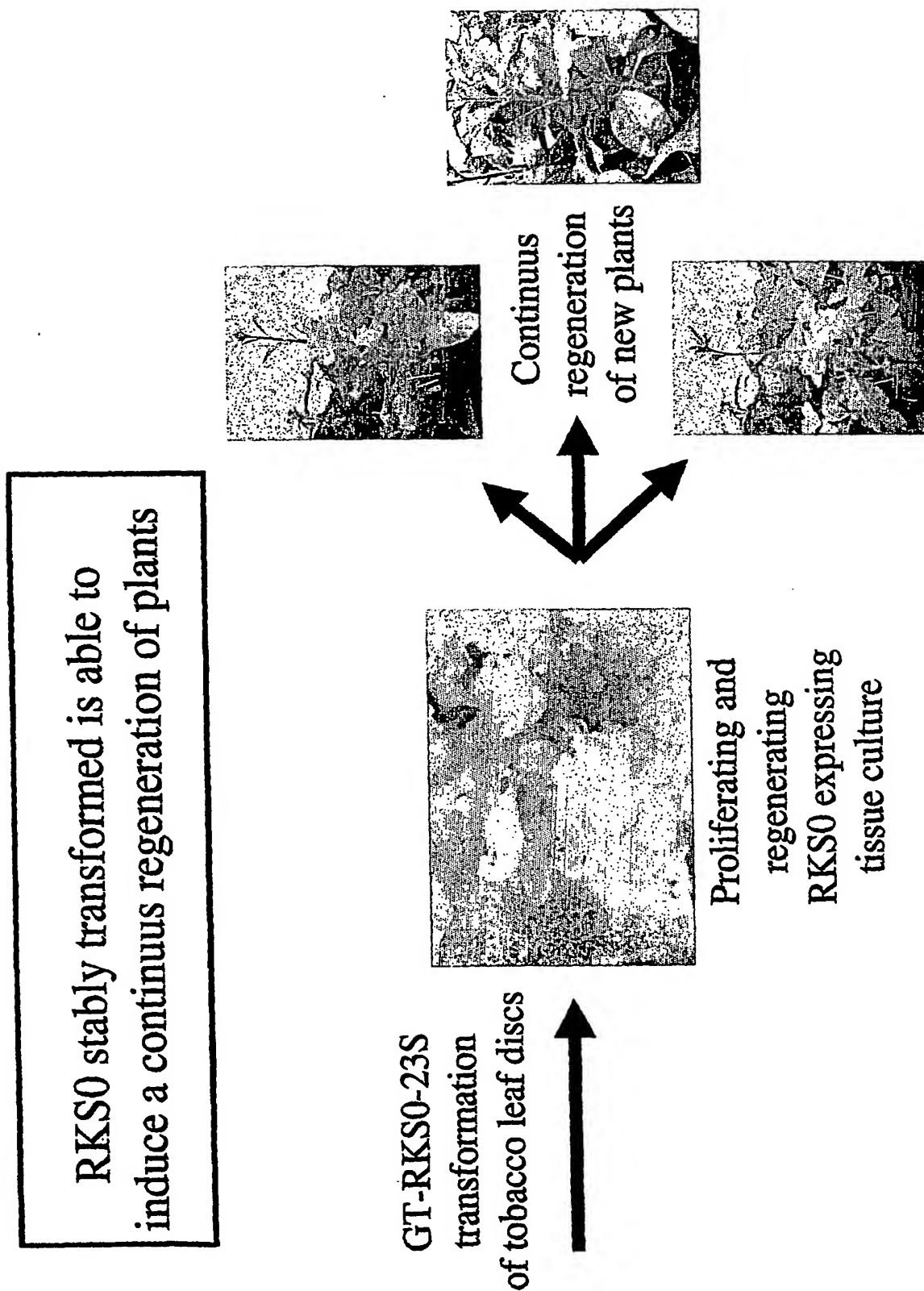


Fig. 19

Fasciation in transgenic
Arabidopsis thaliana

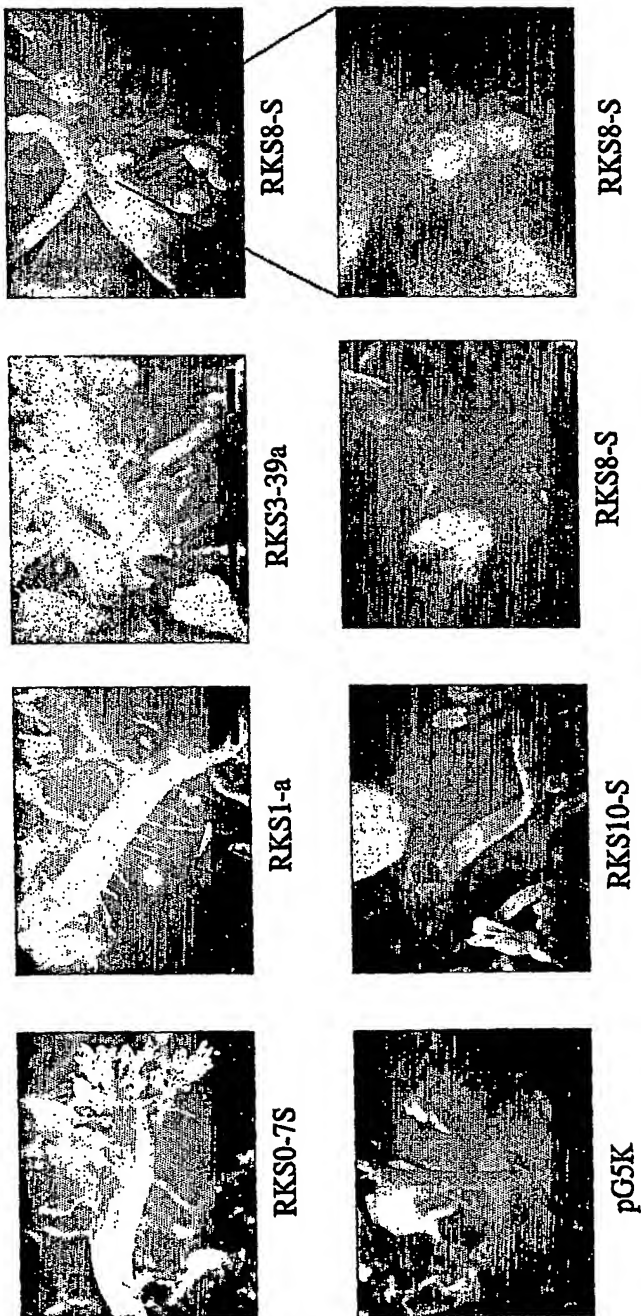


Fig. 20

Root growth of transgenic
Arabidopsis thaliana

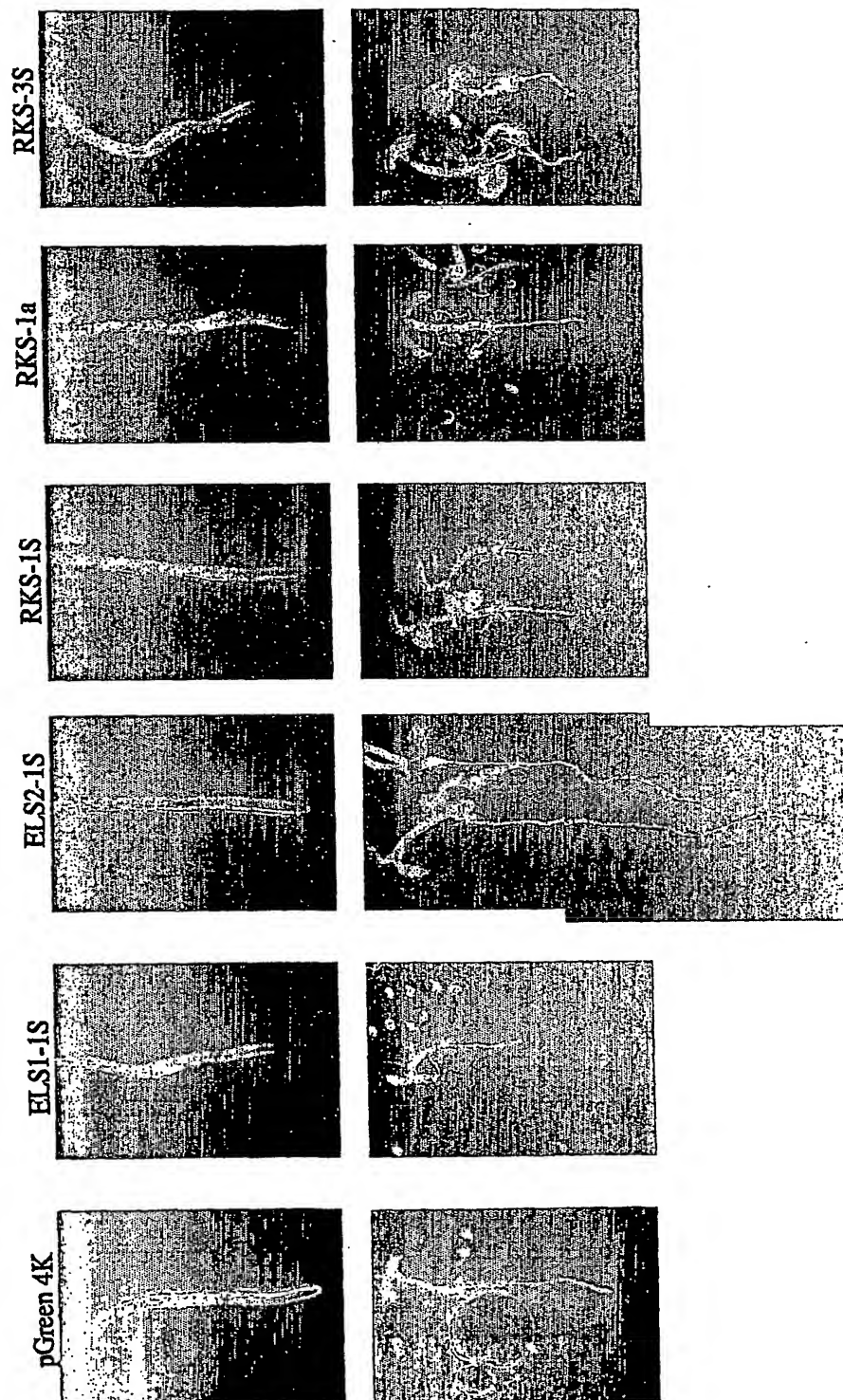


Fig. 21

Root growth of transgenic
Arabidopsis thaliana

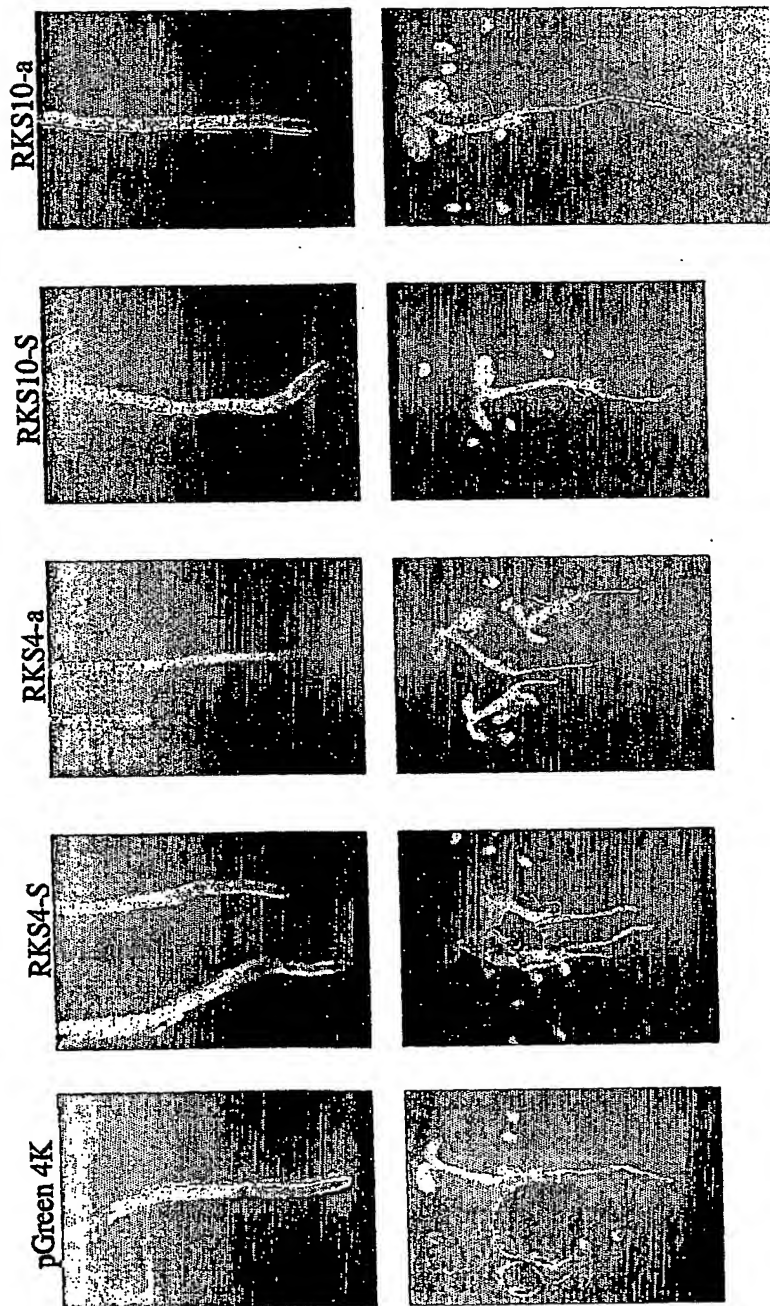


Fig. 22

Root growth of transgenic
Arabidopsis thaliana

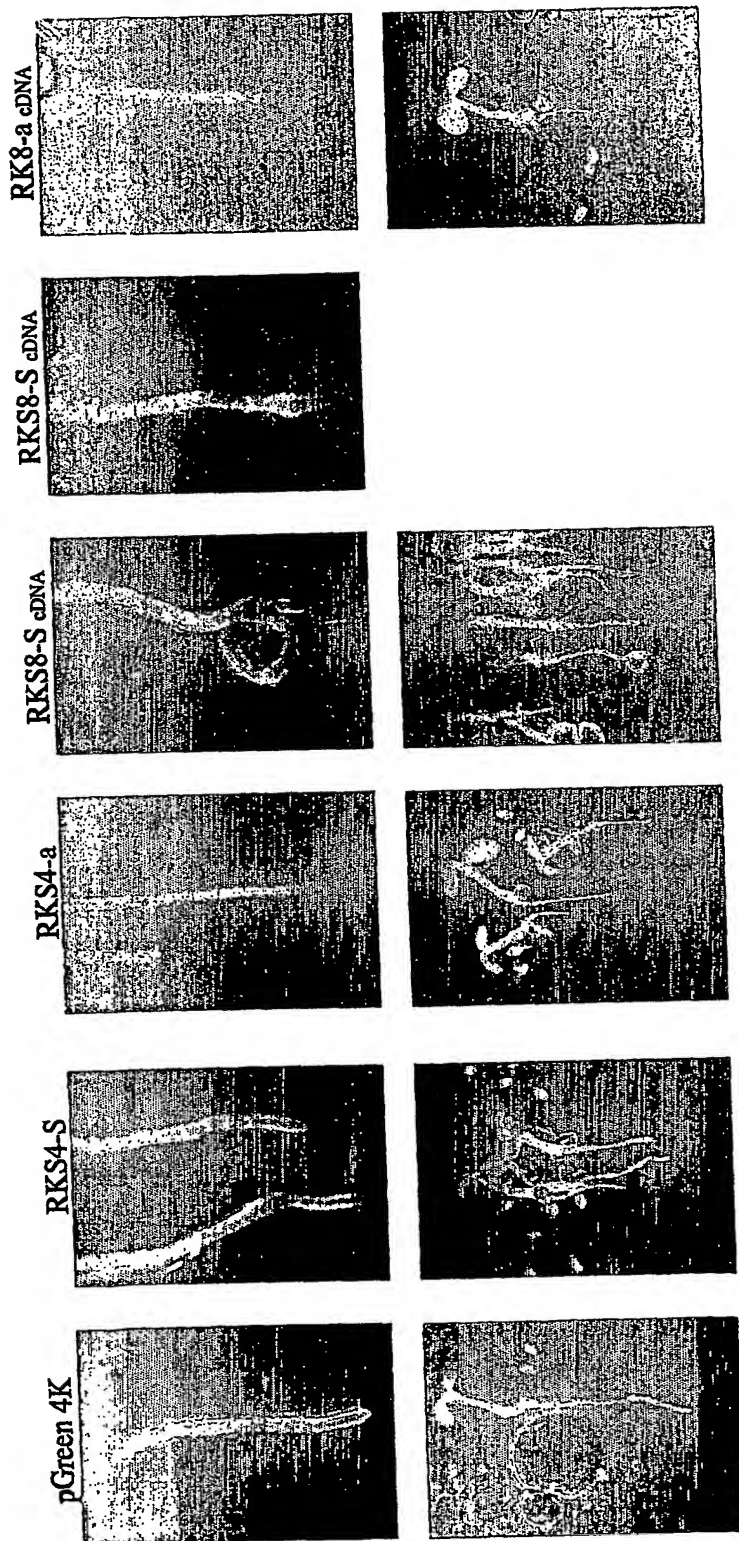


Fig. 23

Root growth of transgenic
Arabidopsis thaliana

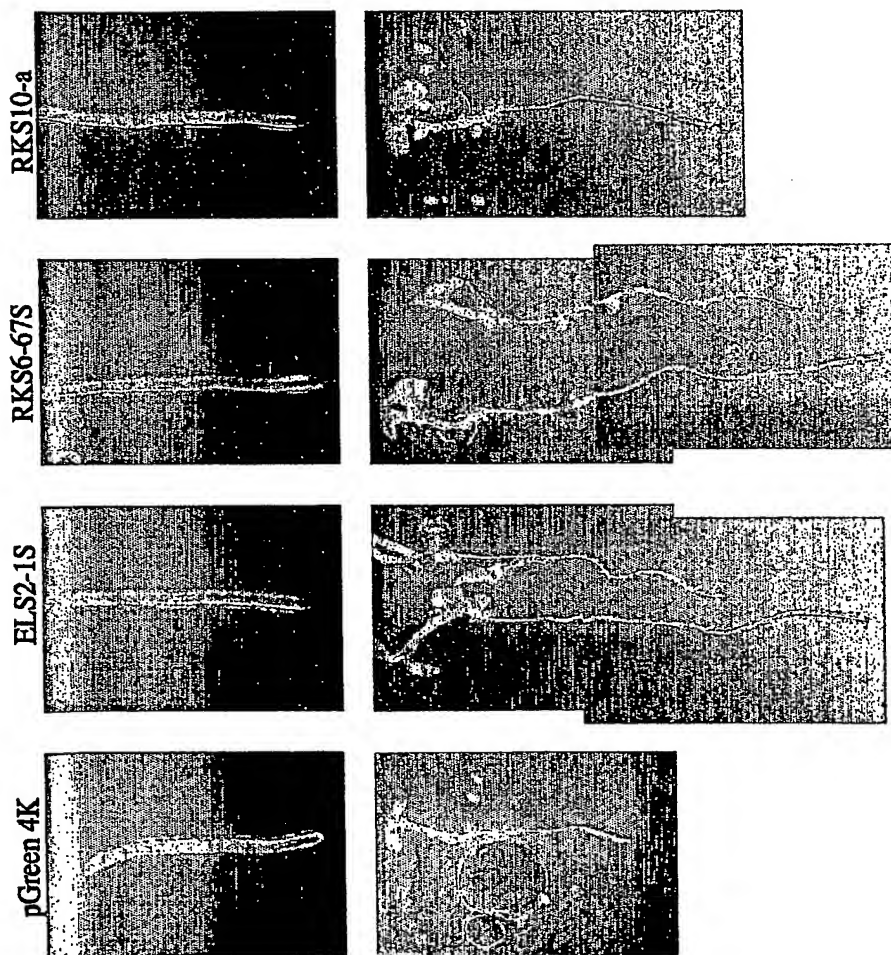


Fig. 24

Transgenic *Arabidopsis thaliana*
primary root length after 14 days
of germination

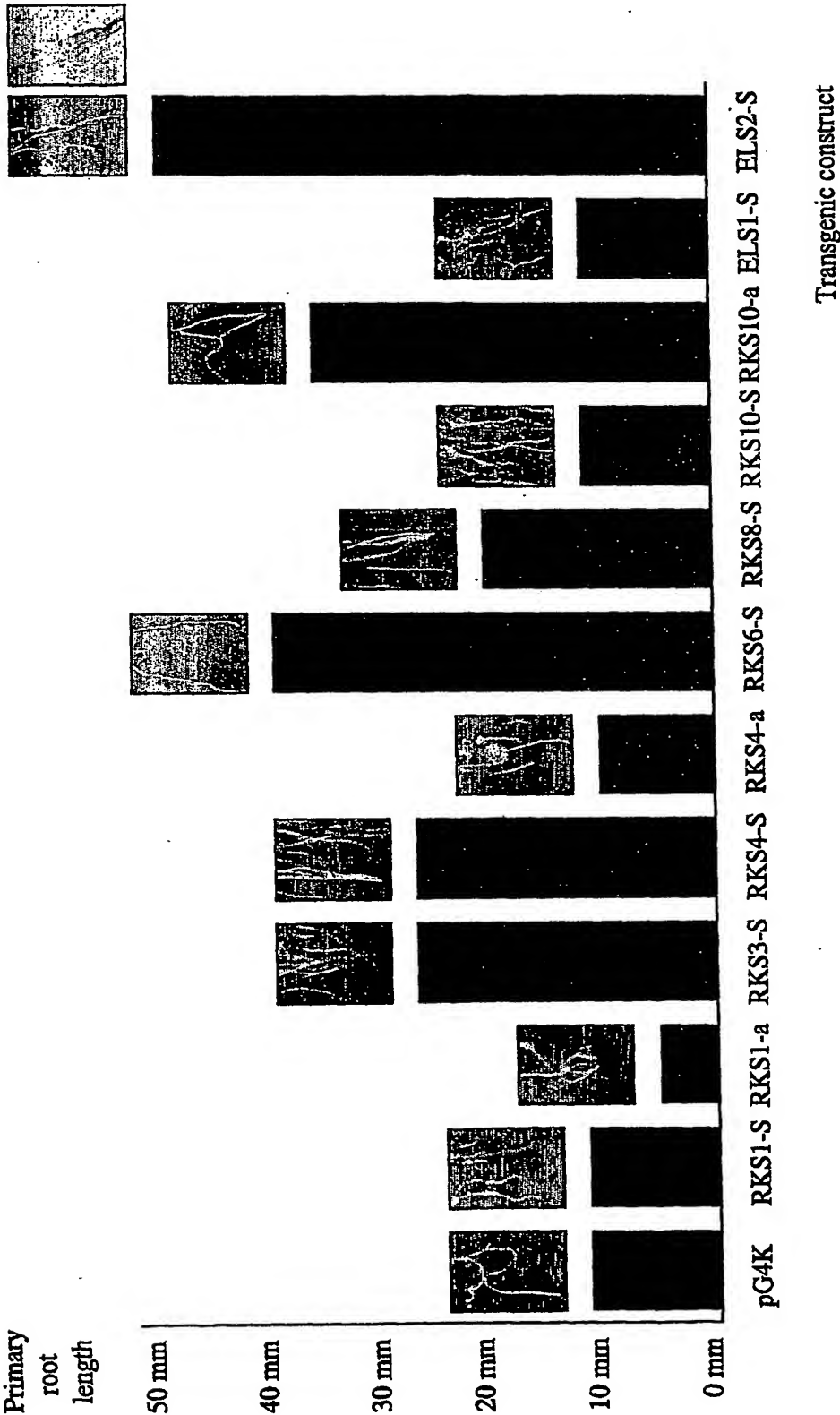


Fig. 25

Effects of RKS10 transgenic
constructs on plant development
of 45 days old *Arabidopsis* WS

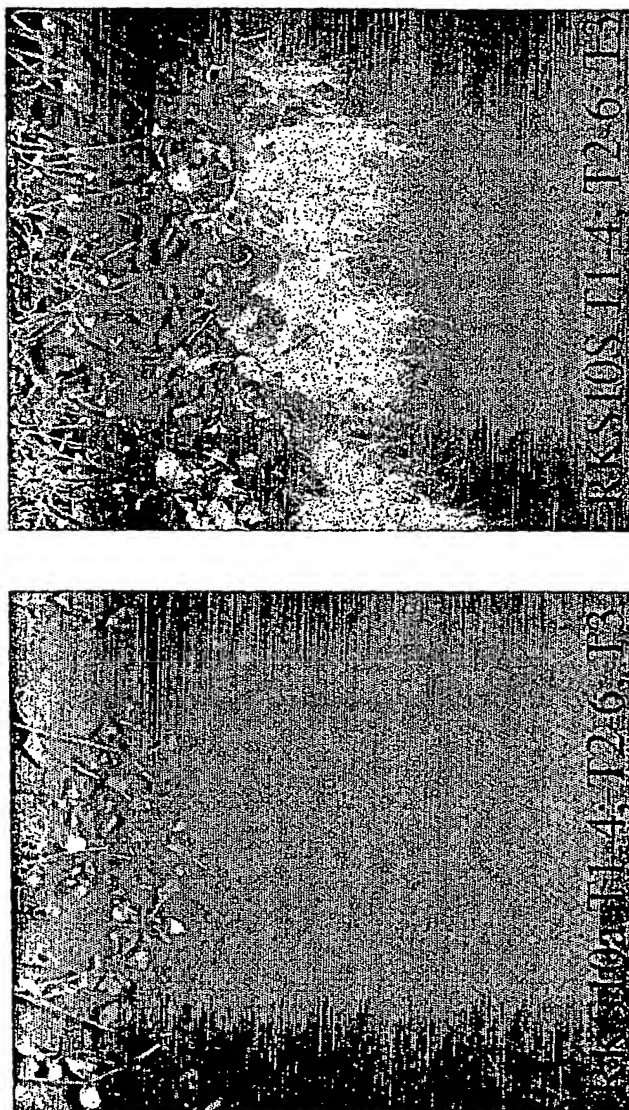


Fig. 26

Roots of Transgenic
Arabidopsis thaliana

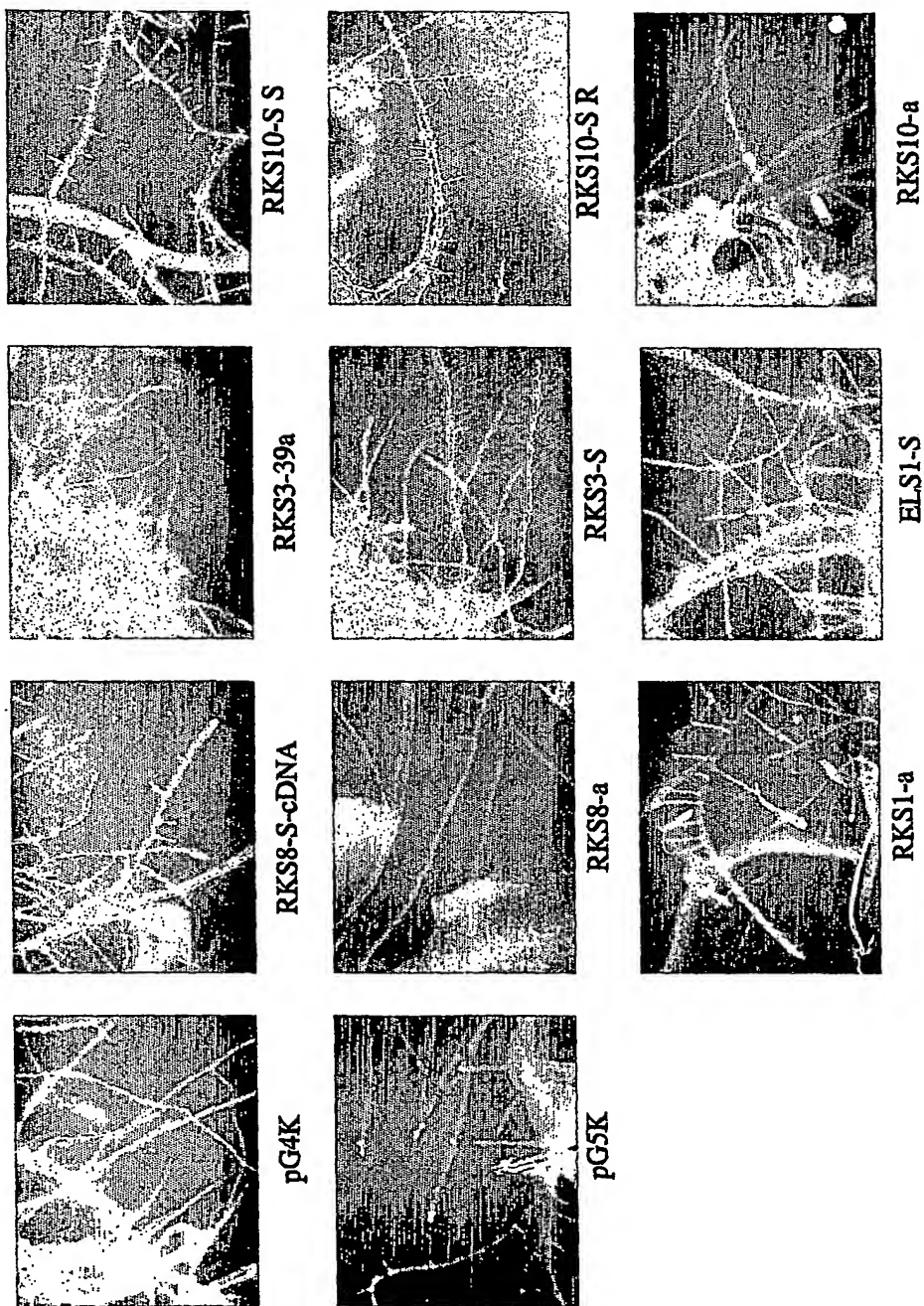


Fig. 27

Root cells of transgenic
Arabidopsis thaliana

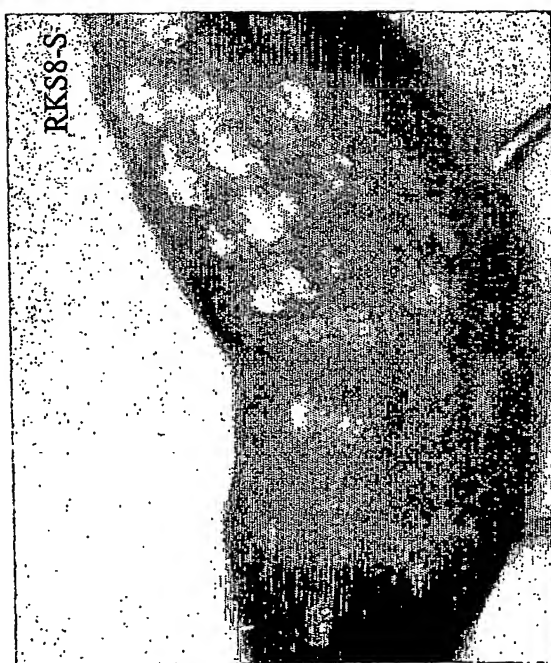
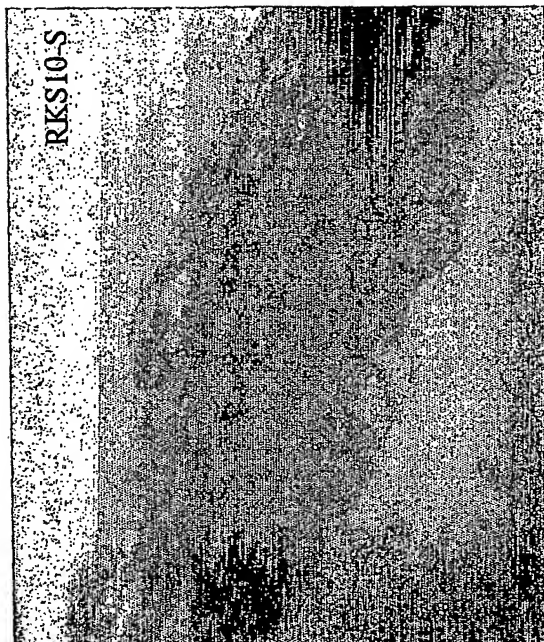


Fig. 28

Influences of T1 transgenic
Arabidopsis WS plants

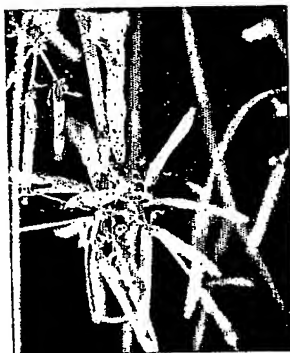
ELS-1-T1



RKS8-a-T1-10



RKS10-a-T2



RKS10-S-T1-10

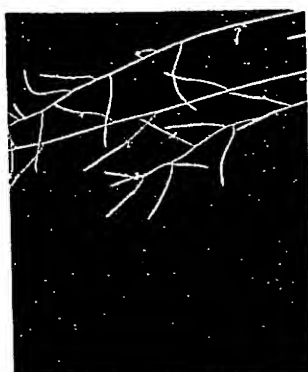


Control pGreen4K

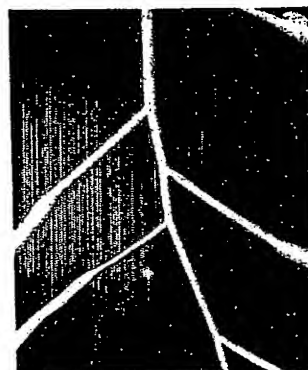


Fig. 29

Influences of T1 transgenic
Arabidopsis WS plants



Control pG4K



RKS8-a-T1-10



RKS10-S-T1-10



Fig. 30

RKS10a T1 expression constructs in
Arabidopsis thaliana

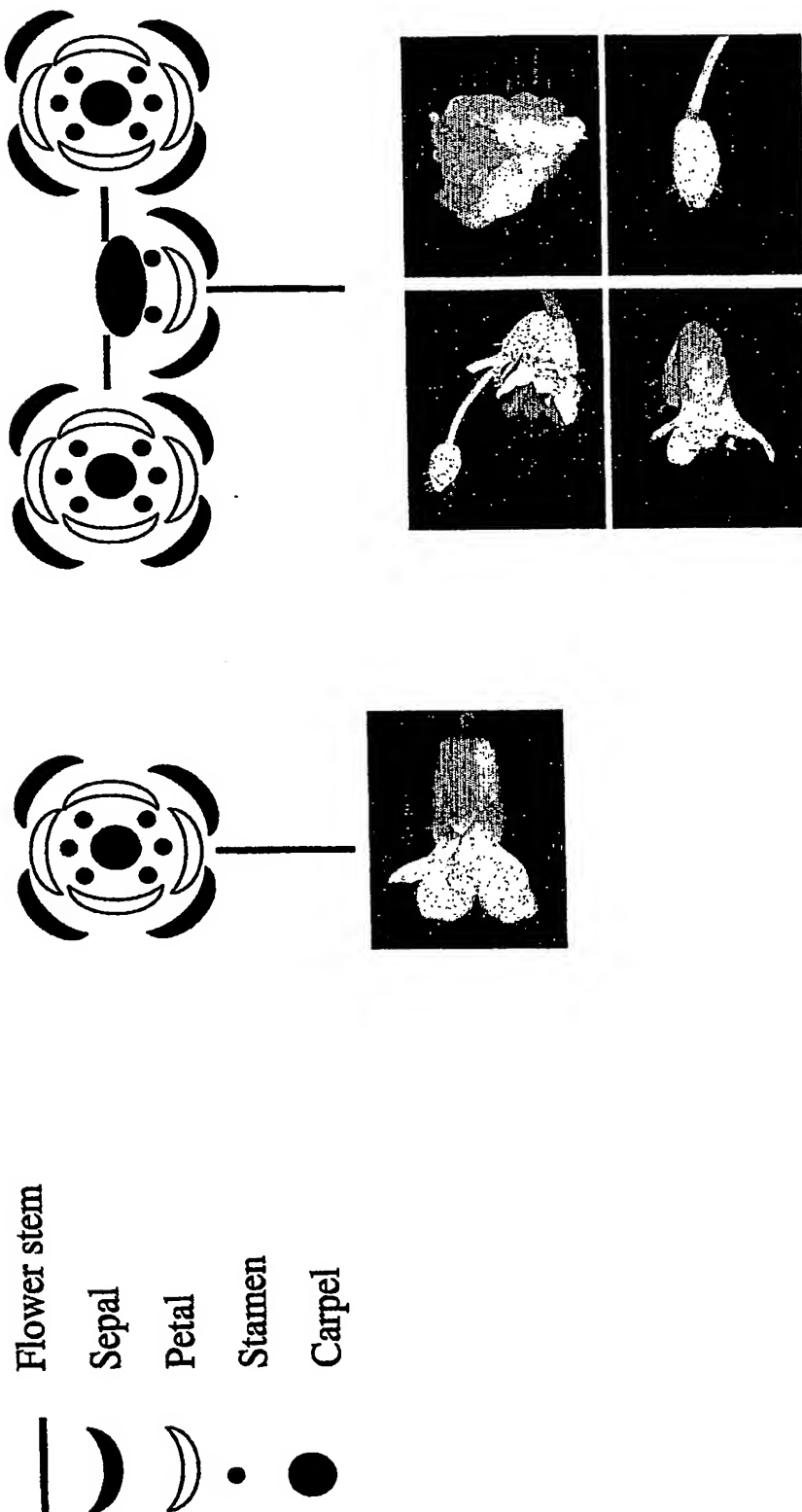


Fig. 31

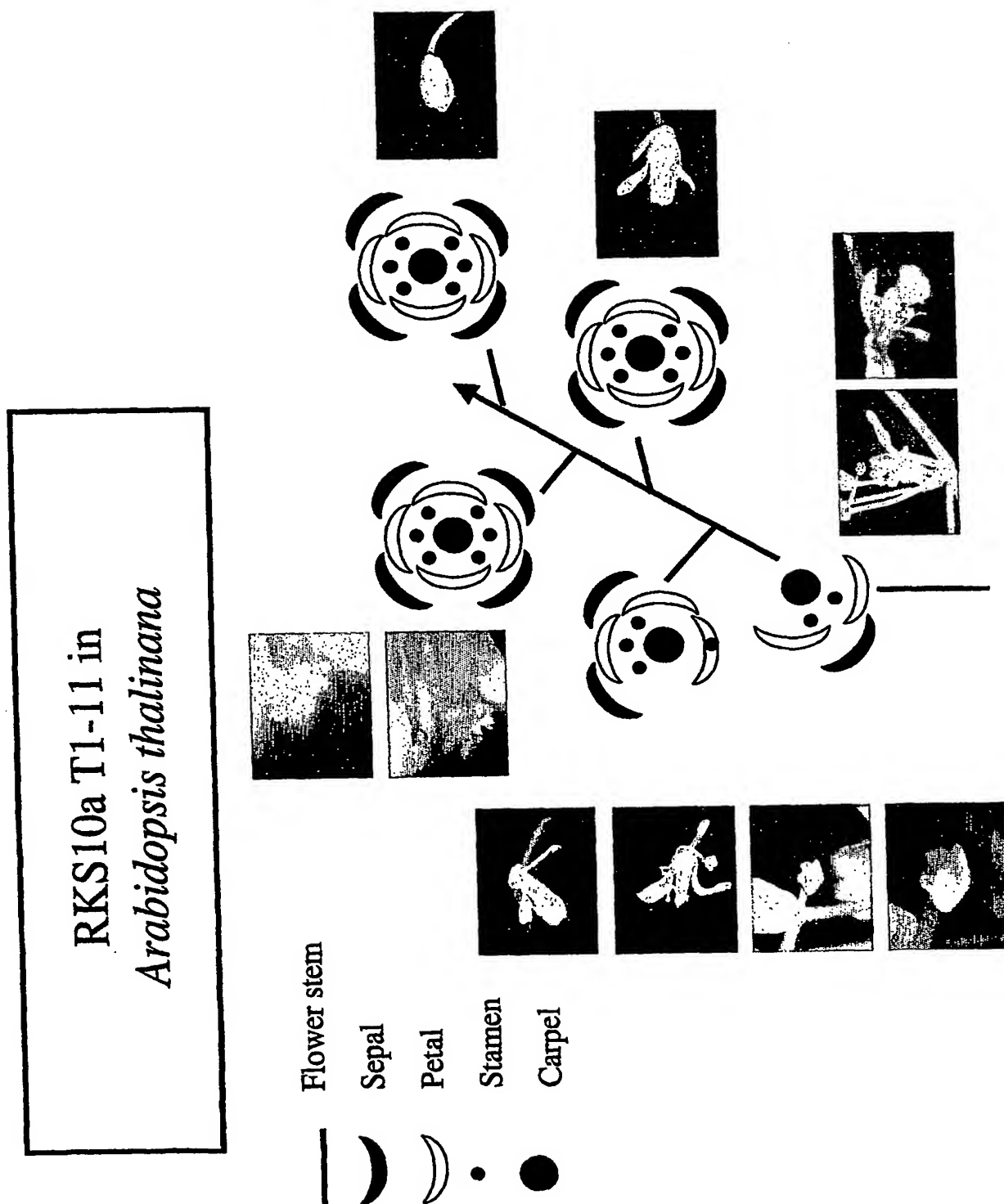
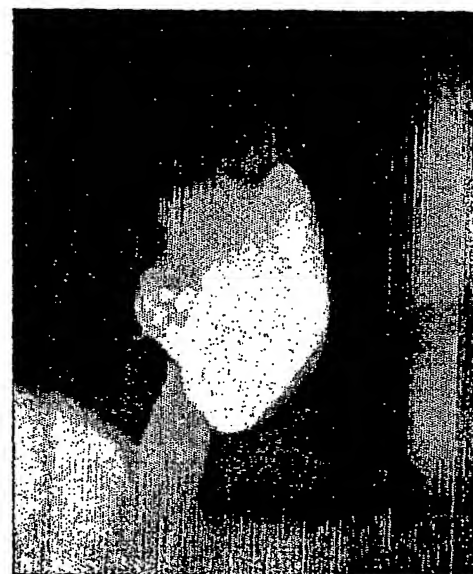


Fig. 32

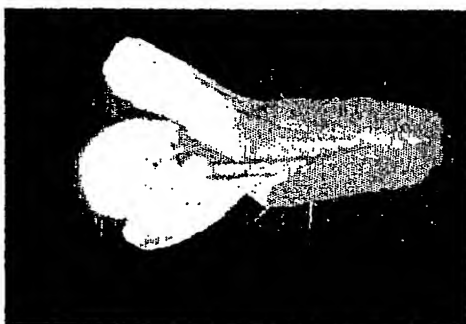
RKS10 antisense effects in
Arabidopsis thaliana



detail flower RKS10a T1-11



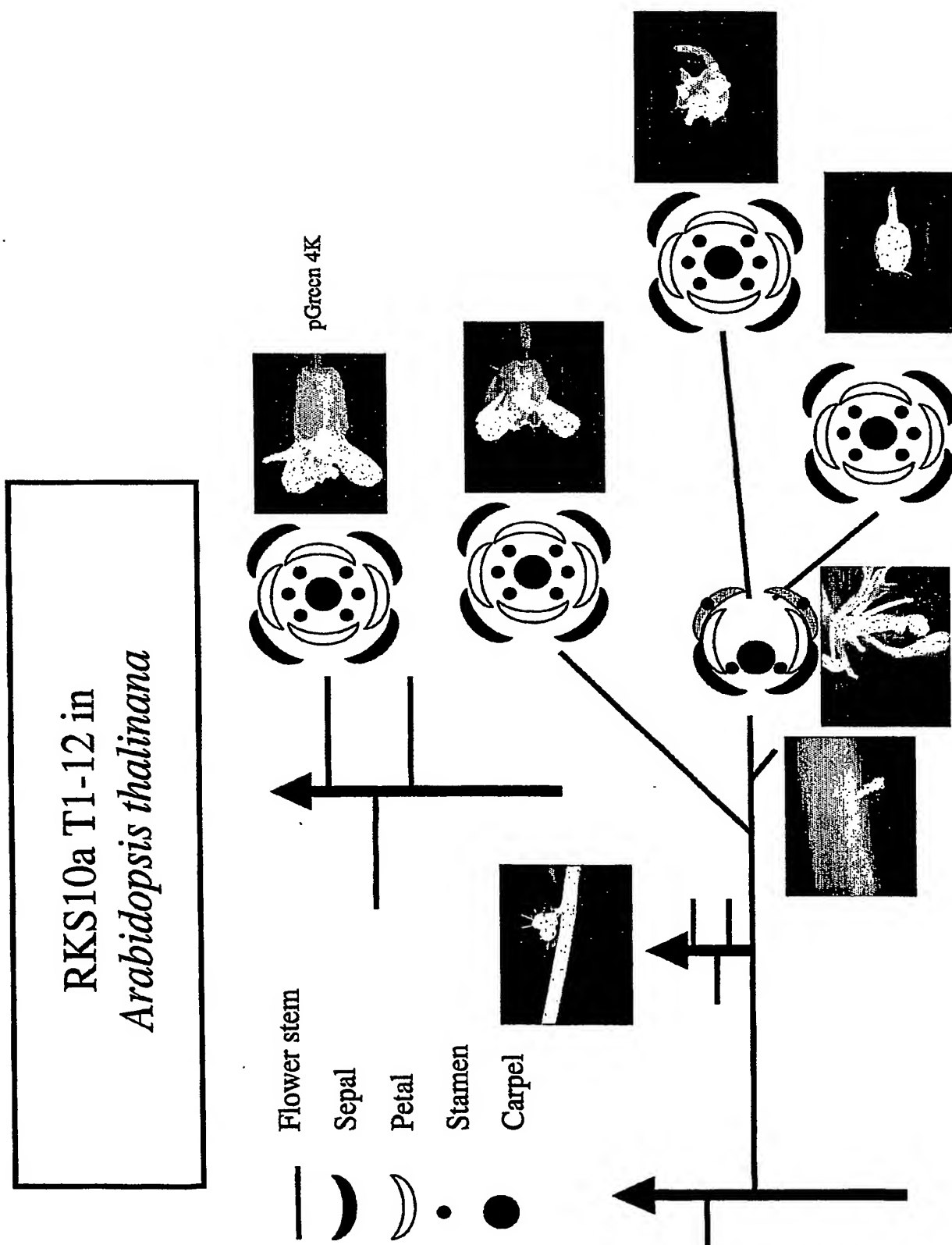
RKS10a T1-11



pGreen 4K



Fig. 33



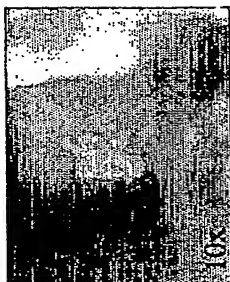


Fig. 35

RKS13 regulates
flower meristem identity in
Arabidopsis thaliana

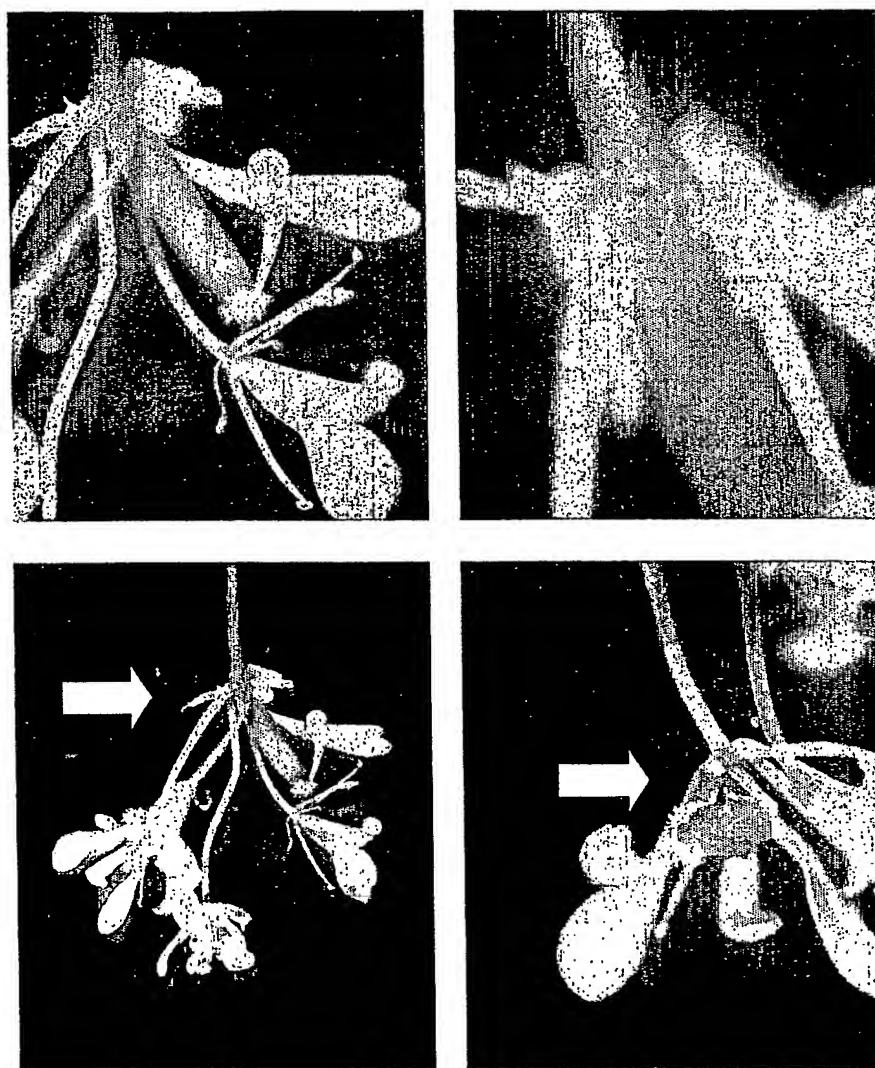
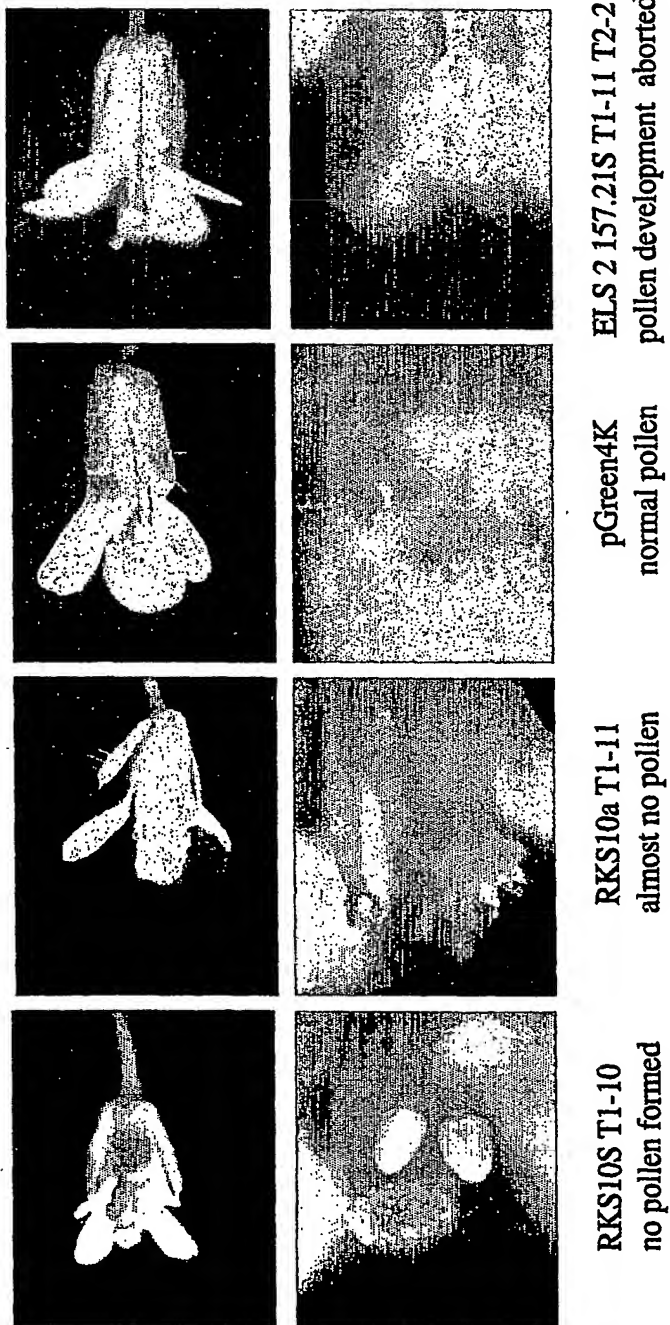


Fig. 36

Male sterile transgenes in
Arabidopsis thaliana



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